```
  1 CGCGTGCAGGTGGCAGTCCTCCCAAAGTACTTGTGTCCGGGTGGT
 46 GGACTGGATTCGCTGCGGAGCCCTGGAAGCTGCCTTTCCTTCTCC

 91 CTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGT
                                MetGlyTrpThrMetArgLeuVa

136 CACAGCAGCACTGTTACTGGGTCTCATGATGGTGGTCACTGGAGA
    lThrAlaAlaLeuLeuLeuGlyLeuMetMetValValThrGlyAs

181 CGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCTTGGACGA
    pGluAspGluAsnSerProCysAlaHisGluAlaLeuLeuAspGl

226 GGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTT
    uAspThrLeuPheCysGlnGlyLeuGluValPheTyrProGluLe

271 GGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAG
    uGlyAsnIleGlyCysLysValValProAspCysAsnAsnTyrAr

316 ACAGAAGATCACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGG
    gGlnLysIleThrSerTrpMetGluProIleValLysPheProGl

361 GGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGGATCCAGA
    yAlaValAspGlyAlaThrTyrIleLeuValMetValAspProAs

406 TGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTG
    pAlaProSerArgAlaGluProArgGlnArgPheTrpArgHisTr

451 GCTGGTAACAGATATCAAGGGCGCCGACCTGAAGGAAGGGAAGAT
    pLeuValThrAspIleLysGlyAlaAspLeuLysGluGlyLysIl

496 TCAGGGCCAGGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGC
    eGlnGlyGlnGluLeuSerAlaTyrGlnAlaProSerProProAl

541 ACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCAGGA
    aHisSerGlyPheHisArgTyrGlnPhePheValTyrLeuGlnGl

586 AGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGG
    uGlyLysValIleSerLeuLeuProLysGluAsnLysThrArgGl

631 CTCTTGGAAAATGGACAGATTTCTGAACCGTTTCCACCTGGGCGA
    ySerTrpLysMetAspArgPheLeuAsnArgPheHisLeuGlyGl

676 ACCTGAAGCAAGCACCCAGTTCATGACCCAGAACTACCAGGACTC
    uProGluAlaSerThrGlnPheMetThrGlnAsnTyrGlnAspSe

721 ACCAACCCTCCAGGCTCCCAGAGAAAGGGCCAGCGAGCCCAAGCA
    rProThrLeuGlnAlaProArgGluArgAlaSerGluProLysHi

766 CAAAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGGCTTTGC
    sLysAsnGlnAlaGluIleAlaAlaCys

811 CATCCGGGCATGTGGCCACACTGCCCACCACCGACGATGTGGGTA
856 TGGAACCCCCTCTGGATACAGAACCCCTTCTTTTCCAAATTAAAA
901 AAAAAAATCATCCAGGAAAAAAAAAAAAAAAA
```

Fig. 1

1 GGAGGTGGGGTGAGACAGGACCAGCCCCTAAGCCTGGTCAGGCCT

46 GATCAAGTGCTGTGGCAGTCATGGTGCGAACGCGGTGGCAGCCTC
MetValArgThrArgTrpGlnProH

91 ACCCTCCGCCGCCCCTGCTTCTCCTGGTGCTCGTGTGGCTCCCCC
isProProProProLeuLeuLeuLeuValLeuValTrpLeuProG

136 AAAGCCTGAGTCTAGACCTGATTGCCTACGTGCCGCAGATAACAG
lnSerLeuSerLeuAspLeuIleAlaTyrValProGlnIleThrA

181 CCTGGGACCTGGAAGGGAAGATCACAGCCACTACATTCTCTCTGG
laTrpAspLeuGluGlyLysIleThrAlaThrThrPheSerLeuG

226 AGCAGCCTCGGTGCGTCTTTGATGAGCATGTCTCAACTAAGGACA
luGlnProArgCysValPheAspGluHisValSerThrLysAspT

271 CCATCTGGCTAGTGGTGGCTTTCAGCAATGCCTCCAGGGACTTTC
hrIleTrpLeuValValAlaPheSerAsnAlaSerArgAspPheG

316 AGAACCCACAGACTGCTGCTAAGATCCCGACCTTCCCACAGCTGC
lnAsnProGlnThrAlaAlaLysIleProThrPheProGlnLeuL

361 TGACTGACGGCCACTATATGACATTACCCCTGTCCCTGGATCAGC
euThrAspGlyHisTyrMetThrLeuProLeuSerLeuAspGlnL

406 TGCCATGTGAGGACCTGACCGGTGGCAGTGGAGGTGTCCCCGTGC
euProCysGluAspLeuThrGlyGlySerGlyGlyValProValL

451 TTCGGGTGGGCAATGATTTTGGCTGTTACCAGCGACCCTATTGCA
euArgValGlyAsnAspPheGlyCysTyrGlnArgProTyrCysA

496 ACGCCCCCCTCCCCAGCCAGGGCCCTTACAGTGTGAAGTTCCTTG
snAlaProLeuProSerGlnGlyProTyrSerValLysPheLeuV

541 TAATGGATGCCGCCGGCCCACCCAAGGCTGAGACGAAGTGGTCCA
alMetAspAlaAlaGlyProProLysAlaGluThrLysTrpSerA

586 ACCCCATTTATCTCCACCAAGGAAAGAATCCCAACTCCATTGACA
snProIleTyrLeuHisGlnGlyLysAsnProAsnSerIleAspT

631 CATGGCCTGGCCGACGGAGCGGCTGTATGATCGTCATAACTTCCA
hrTrpProGlyArgArgSerGlyCysMetIleValIleThrSerI

676 TCCTCTCTGCCCTGGCCGGCCTCTTGCTCCTGGCTTTCCTGGCAG
leLeuSerAlaLeuAlaGlyLeuLeuLeuLeuAlaPheLeuAlaA

721 CTTCCACTACGCGT
laSerThrThrArg

Fig. 2

```
  1 AAAGAGCTTGAGTTAGATTGAAGTAGAATCAGTGATAGAAAATAA
 46 CAGCCGAAAACAAACAAAAAGGGGACATAGTGACAATTTCTCCTG
 91 GGTTATTTTGGCTGGAACCAACTTCCATTATCCAGAAGCTGATAA
136 AAAAGCTTTGGGAAACATGAACAAAACATTGATGAAATGTTGGAA
181 ACCAGTTGAAACACAGTAAAACCAACTGGGTAAAATAGGACCACT

226 TCTCTTCATCTACACTGGGATTTGTCAAGAAGTGAACTATGACAA
                                           MetThrI

271 TACATCAATTTTTGCTACTGTTTCTATTCTGGGTATGCCTGCCAC
    leHisGlnPheLeuLeuLeuPheLeuPheTrpValCysLeuProH

316 ATTTCTGCTCTCCAGAAATAATGTTCAGAAGGACGCCTGTGCCAC
    isPheCysSerProGluIleMetPheArgArgThrProValProG

361 AGCAAAGAATTTTAAGTTCACGTGTACCAAGGAGTGATGGCAAAA
    lnGlnArgIleLeuSerSerArgValProArgSerAspGlyLysI

406 TTCTCCATCGTCAAAAACGTGGTTGGATGTGGAATCAATTTTTCT
    leLeuHisArgGlnLysArgGlyTrpMetTrpAsnGlnPhePheL

451 TACTTGAAGAATATACAGGATCTGATTATCAGTACGTAGGCAAGC
    euLeuGluGluTyrThrGlySerAspTyrGlnTyrValGlyLysL

496 TACATTCAGACCAAGATAAAGGAGATGGATCACTCAAATATATCT
    euHisSerAspGlnAspLysGlyAspGlySerLeuLysTyrIleL

541 TATCTGGAGATGGAGCTGGTACTCTTTTTATTATTGATGAAAAAA
    euSerGlyAspGlyAlaGlyThrLeuPheIleIleAspGluLysT

586 CAGGTGATATTCATGCCACAAGGCGAATTGATAGGGAGGAAAAGG
    hrGlyAspIleHisAlaThrArgArgIleAspArgGluGluLysA

631 CCTTTTATACTCTACGCGCACAAGCTATTAACAGAAGAACTCTGA
    laPheTyrThrLeuArgAlaGlnAlaIleAsnArgArgThrLeuA

676 GGCCAGTAGAGCCAGAGTCAGAGTTTGTGATCAAAATTCATGATA
    rgProValGluProGluSerGluPheValIleLysIleHisAspI

721 TCAATGACAATGAGCCAACGTTCCCAGAAGAAATCTATACAGCTA
    leAsnAspAsnGluProThrPheProGluGluIleTyrThrAlaS

766 GTGTTCCCGAAATGTCTGTTGTAGGTACTTCTGTGGTGCAAGTCA
    erValProGluMetSerValValGlyThrSerValValGlnValT

811 CAGCTACAGATGCCGATGACCCTTCATATGGGAACAGCGCCAGAG
    hrAlaThrAspAlaAspAspProSerTyrGlyAsnSerAlaArgV

856 TCATTTACAGCATACTTCAAGGGCAGCCCTATTTCTCTGTGGAGC
    alIleTyrSerIleLeuGlnGlyGlnProTyrPheSerValGluP

901 CTGAAACAGGTATCATCAGGACTGCTTTACCGAACATGAACAGAG
    roGluThrGlyIleIleArgThrAlaLeuProAsnMetAsnArgG
```

Fig. 3

946 AAAACAGAGAGCAATACCAAGTGGTCATCCAGGCCAAAGACATGG
luAsnArgGluGlnTyrGlnValValIleGlnAlaLysAspMetG

991 GCGGCCAGATGGGAGGCTTATCGGGGACAACCACTGTGAACATCA
lyGlyGlnMetGlyGlyLeuSerGlyThrThrThrValAsnIleT

1036 CGCTGACAGATGTCAATGACAACCCACCACGTTTCCCCCAGAACA
hrLeuThrAspValAsnAspAsnProProArgPheProGlnAsnT

1081 CTATTCATCTTCGAGTTCTTGAATCCTCCCCAGTTGGCACAGCCA
hrIleHisLeuArgValLeuGluSerSerProValGlyThrAlaI

1126 TTGGAAGTGTCAAAGCAACTGATGCTGACACTGGGAAAAATGCTG
leGlySerValLysAlaThrAspAlaAspThrGlyLysAsnAlaG

1171 AAGTAGAATACCGAATTATTGATGGTGACGGTACTGATATGTTTG
luValGluTyrArgIleIleAspGlyAspGlyThrAspMetPheA

1216 ACATCGTGACTGAGAAGGACACACAGGAAGGCATCATCACTGTGA
spIleValThrGluLysAspThrGlnGluGlyIleIleThrValL

1261 AAAAGCCACTCGACTATGAAAGCCGAAGACTTTATACTCTGAAAG
ysLysProLeuAspTyrGluSerArgArgLeuTyrThrLeuLysV

1306 TCGAAGCAGAAAACACCCATGTAGATCCCCGTTTTTATTACCTAG
alGluAlaGluAsnThrHisValAspProArgPheTyrTyrLeuG

1351 GACCATTTAAAGATACTACCATAGTGAAAATCTCTATAGAAGATG
lyProPheLysAspThrThrIleValLysIleSerIleGluAspV

1396 TGGATGAACCTCCTGTTTTTAGTAGGTCCTCCTATCTGTTTGAAG
alAspGluProProValPheSerArgSerSerTyrLeuPheGluV

1441 TTCATGAAGATATTGAAGTGGGCACAATCATTGGTACTGTAATGG
alHisGluAspIleGluValGlyThrIleIleGlyThrValMetA

1486 CAAGGGACCCAGATTCTATTTCCAGCCCCATTAGATTTTCCTTGG
laArgAspProAspSerIleSerSerProIleArgPheSerLeuA

1531 ATCGCCATACTGACCTTGACAGAATCTTTAACATTCATTCAGGAA
spArgHisThrAspLeuAspArgIlePheAsnIleHisSerGlyA

1576 ATGGATCTCTTTATACATCAAAACCTCTTGACCGTGAACTATCTC
snGlySerLeuTyrThrSerLysProLeuAspArgGluLeuSerG

1621 AGTGGCATAATTCGTTAGTTATTGCTGCTGAAATCAACAATCCCA
lnTrpHisAsnSerLeuValIleAlaAlaGluIleAsnAsnProL

1666 AAGAGACAACACGCGTGGCTGTTTTTGTGAGAATTTTGGATGTTA
ysGluThrThrArgValAlaValPheValArgIleLeuAspValA

1711 ATGACAATGCCCCACAGTTTGCTGTGTTCTATGACACTTTTGTAT
snAspAsnAlaProGlnPheAlaValPheTyrAspThrPheValC

1756 GTGAAAATGCCAGACCAGGGCAGCTAATACAGACTATAAGTGCAG
ysGluAsnAlaArgProGlyGlnLeuIleGlnThrIleSerAlaV

Fig. 3 Continued

```
1801 TAGACAAAGATGACCCTTTAGGTGGACAGAAATTTTTTTCAGTT
     alAspLysAspAspProLeuGlyGlyGlnLysPhePhePheSerL

1846 TAGCTGCTGTCAATCCAAACTTCACAGTACAGGATAATGAAGATA
     euAlaAlaValAsnProAsnPheThrValGlnAspAsnGluAspA

1891 ATACTGCCAGAATCTTAACCAGAAAAAATGGATTCAATAGACATG
     snThrAlaArgIleLeuThrArgLysAsnGlyPheAsnArgHisG

1936 AAATCAGTACCTATCTCTTGCCTGTGGTGATATCAGACAATGATT
     luIleSerThrTyrLeuLeuProValValIleSerAspAsnAspT

1981 ACCCGATTCAGAGCAGCACAGGCACACTGACCATTCGAGTGTGTG
     yrProIleGlnSerSerThrGlyThrLeuThrIleArgValCysA

2026 CTTGTGACAGCCAAGGCAACATGCAATCCTGCAGTGCTGAAGCCC
     laCysAspSerGlnGlyAsnMetGlnSerCysSerAlaGluAlaL

2071 TGCTCCTCCCTGCCGGCCTCAGCACTGGGGCCTTGATCGCCATCC
     euLeuLeuProAlaGlyLeuSerThrGlyAlaLeuIleAlaIleL

2116 TCCTCTGCATCATCATTCTACTGGTTATAGTAGTACTGTTTGCAG
     euLeuCysIleIleIleLeuLeuValIleValValLeuPheAlaA

2161 CTCTGAAAGGACAGCGAAAAAAAGAGCCTCTGATCTTGTCAAAAG
     laLeuLysGlyGlnArgLysLysGluProLeuIleLeuSerLysG

2206 AAGATATCAGAGACAACATTGTGAGCTATAACGATGAGGGTGGTG
     luAspIleArgAspAsnIleValSerTyrAsnAspGluGlyGlyG

2251 GAGAGGAGGACACCCAGGCCTTTGATATCGGCACCCTGAGGAATC
     lyGluGluAspThrGlnAlaPheAspIleGlyThrLeuArgAsnP

2296 CTGCAGCCATTGAGGAAAAAAAGCTCCGGCGAGATATTATTCCAG
     roAlaAlaIleGluGluLysLysLeuArgArgAspIleIleProG

2341 AAACGTTATTTATTCCTCGGAGGACTCCTACAGCTCCAGATAACA
     luThrLeuPheIleProArgArgThrProThrAlaProAspAsnT

2386 CGGACGTCCGGGATTTCATTAATGAAAGGCTAAAAGAGCATGATC
     hrAspValArgAspPheIleAsnGluArgLeuLysGluHisAspL

2431 TTGACCCCACCGCACCCCCCTACGACTCACTTGCAACCTATGCCT
     euAspProThrAlaProProTyrAspSerLeuAlaThrTyrAlaT

2476 ATGAAGGAAATGATTCCATTGCTGAATCTCTGAGTTCATTAGAAT
     yrGluGlyAsnAspSerIleAlaGluSerLeuSerSerLeuGluS

2521 CAGGTACTACTGAAGGAGACCAAAACTACGATTACCTCCGAGAAT
     erGlyThrThrGluGlyAspGlnAsnTyrAspTyrLeuArgGluT

2566 GGGGCCCTCGGTTTAATAAGCTAGCAGAAATGTATGGTGGTGGGG
     rpGlyProArgPheAsnLysLeuAlaGluMetTyrGlyGlyGlyG

2611 AAAGTGACAAAGACTCTTAACGTAGGATATATGTTCTGTTCAAAC
     luSerAspLysAspS r

2656 AAGAGAAAGTAACTCTACCCATGCTGTCTCCACTTCACAATATTT
2701 GATATTCAGGAGCATTTCCTGCAGTCAGCACAATTTTTTTCTCA
```

Fig. 3 Continued

```
  1 AAGATGGTAGCAAAGTAATGAGTTGAGAGTTGCTTTCAGTGGTGT
 46 GTTACCGGAGATAGAAAAAATGAAGGATACAGGCTAAGGGACCAA
 91 CTGCAGTGTGATGGAAACTGAGTTTTAATGATGCCTCTTAGGAAA
136 TGACTTCCAACATGTAGTACACTATTCATCTTCGAGTTCTTGAAT
181 CCTCCCCAGTTGGCACAGCCATTGGAAGTGTCAAAGCAACTGATG
226 CTGACACTGGGAAAAATGCTGAAGTAGAATACCGAATTATTGATG

271 GTGACGGTACTGATATGTTTGACATCGTGACTGAGAAGGACACAC
                  MetPheAspIleValThrGluLysAspThrG

316 AGGAAGGCATCATCACTGTGAAAAAGCCACTCGACTATGAGAGCC
    lnGluGlyIleIleThrValLysLysProLeuAspTyrGluSerA

361 GAAGACTTTATACTCTGAAAGTCGAAGCAGAAAACACCCATGTAG
    rgArgLeuTyrThrLeuLysValGluAlaGluAsnThrHisvalA

406 ATCCCCGTTTTTATTACCTAGGACCATTTAAAGATACTACCATAG
    spProArgPheTyrTyrLeuGlyProPheLysAspThrThrIleV

451 TGAAAATCTCTATAGAAGATGTGGATGAACCTCCTGTTTTTAGTA
    alLysIleSerIleGluAspValAspGluProProValPheSerA

496 GGTCCTCCTATCTGTTTGAAGTTCATGAAGATATTGAAGTGGGCA
    rgSerSerTyrLeuPheGluValHisGluAspIleGluValGlyT

541 CAATCATTGGTACTGTAATGGCAAGGGACCCAGATTCTATTTCCA
    hrIleIleGlyThrValMetAlaArgAspProAspSerIleSerS

586 GCCCCATTAGATTTTCCTTGGATCGCCATACTGACCTTGACAGAA
    erProIleArgPheSerLeuAspArgHisThrAspLeuAspArgI

631 TCTTTAACATTCATTCAGGAAATGGATCTCTTTATACATCAAAAC
    lePheAsnIleHisSerGlyAsnGlySerLeuTyrThrSerLysP

676 CTCTTGACCGTGAACTATCTCAGTGGCATAATTCGTTAGTTATTG
    roLeuAspArgGluLeuSerGlnTrpHisAsnSerLeuValIleA

721 CTGCTGAAATCAACAATCCCAAAGAGACAACACGCGTGGCTGTTT
    laAlaGluIleAsnAsnProLysGluThrThrArgValAlaValP

766 TTGTGAGAATTTTGGATGTTAATGACAATGCCCCACAGTTTGCTG
    heValArgIleLeuAspValAsnAspAsnAlaProGlnPheAlaV

811 TGTTCTATGACACTTTTGTATGTGAAAATGCCAGACCAGGGCAGC
    alPheTyrAspThrPheValCysGluAsnAlaArgProGlyGlnL

856 TAATACAGACTATAAGTGCAGTAGACAAAGATGACCCTTTAGGTG
    euIleGlnThrIleSerAlaValAspLysAspAspProLeuGlyG

901 GACAGAAATTTTTTTTCAGTTTAGCTGCTGTCAATCCAAACTTCA
    lyGlnLysPhePhePheSerLeuAlaAlaValAsnProAsnPheT

946 CAGTACAGGATAATGAAGATAATACTGCCAGAATCTTAACCAGAA
    hrValGlnAspAsnGluAspAsnThrAlaArgIleLeuThrArgL
```

Fig. 4

```
991  AAAATGGATTCAATAGACATGAAATCAGTACCTATCTCTTGCCTG
     ysAsnGlyPheAsnArgHisGluIleS rThrTyrLeuLeuProV

1036 TGGTGATATCAGACAATGATTACCCGATTCAGAGCAGCACAGGCA
     alValIleSerAspAsnAspTyrProIleGlnSerSerThrGlyT

1081 CACTGACCATTCGAGTGTGTGCTTGTGACAGCCAAGGCAACATGC
     hrLeuThrIleArgValCysAlaCysAspSerGlnGlyAsnMetG

1126 AATCCTGCAGTGCTGAAGCCCTGCTCCTCCCTGCCGGCCTCAGCA
     lnSerCysSerAlaGluAlaLeuLeuLeuProAlaGlyLeuSerT

1171 CTGGGGCCTTGATCGCCATCCTCCTCTGCATCATCATTCTACTGG
     hrGlyAlaLeuIleAlaIleLeuLeuCysIleIleIleLeuLeuV

1216 TTATAGTAGTACTGTTTGCAGCTCTGAAAGGACAGCGAAAAAAAG
     alIleValValLeuPheAlaAlaLeuLysGlyGlnArgLysLysG

1261 AGCCTCTGATCTTGTCAAAAGAAGATATCAGAGACAACATTGTGA
     luProLeuIleLeuSerLysGluAspIleArgAspAsnIleValS

1306 GCTATAACGATGAGGGTGGTGGAGAGGAGGACACCCAGGCCTTTG
     erTyrAsnAspGluGlyGlyGlyGluGluAspThrGlnAlaPheA

1351 ATATCGGCACCCTGAGGAATCCTGCAGCCATTGAGGAAAAAAAGC
     spIleGlyThrLeuArgAsnProAlaAlaIleGluGluLysLysL

1396 TCCGGCGAGATATTATTCCAGAAACGTTATTTATTCCTCGGAGGA
     euArgArgAspIleIleProGluThrLeuPheIleProArgArgT

1441 CTCCTACAGCTCCAGATAACACGGACGTCCGGGATTTCATTAATG
     hrProThrAlaProAspAsnThrAspValArgAspPheIleAsnG

1486 AAAGGCTAAAAGAGCATGATCTTGACCCCACCGCACCCCCCTACG
     luArgLeuLysGluHisAspLeuAspProThrAlaProProTyrA

1531 ACTCACTTGCAACCTATGCCTATGAAGGAAATGATTCCATTGCTG
     spSerLeuAlaThrTyrAlaTyrGluGlyAsnAspSerIleAlaG

1576 AATCTCTGAGTTCATTAGAATCAGGTACTACTGAAGGAGACCAAA
     luSerLeuSerSerLeuGluSerGlyThrThrGluGlyAspGlnA

1621 ACTACGATTACCTCCGAGAATGGGGCCCTCGGTTTAATAAGCTAG
     snTyrAspTyrLeuArgGluTrpGlyProArgPheAsnLysLeuA

1666 CAGAAATGTATGGTGGTGGGGAAAGTGACAAAGACTCTTAACGTA
     laGluMetTyrGlyGlyGlyGluSerAspLysAspSer

1711 GGATATATGTTCTGTTCAAACAAGAGAAAGTAACTCTACCCATGC
1756 TGTCTCCACTTCACAATATTTGATATTCAGGAGCATTTCCTGCAG
1801 TCAGCACAATTTTTTTCTCA
```

Fig. 4 Continued

```
  1 CAAAGGCTGGAGACAAGTGGGTTGGGGGTTGGTTTTAATTTGGCA
 46 GTTGTAATTAATGGTCAATTTTAATAGTCCGTAATTGATGGCAGC
 91 CTGCTGTGGTACATGTGTGAAAGATTATCACTTTGAATATACGGA
136 ATGTGATAGCAGTGGCTCCAGGTGGAGAGTTGCCATTCCAAATTC
181 TGCAGTGGACTGCTCTGGCCTGCCTGACCCAGTGAGAGGCAAAGA

226 ATGCACTCTTCTTGGATCCCTCGTGGAAACTACATAGAATCTAAT
    MetHisSerSerTrpIleProArgGlyAsnTyrIleGluSerAsn

271 CGTGATGACTGCACGGTGTCTTTGATCTATGCTGTGCACCTTAAG
    ArgAspAspCysThrValSerLeuIleTyrAlaValHisLeuLys

316 AAGTCAGGCTATGTCTTCTTTGAGTACCAGTATGTCGACAACAAC
    LysSerGlyTyrValPhePheGluTyrGlnTyrValAspAsnAsn

361 ATCTTCTTTGAGTTCTTTATTCAAAATGATCAGTGCCAGGAGATG
    IlePhePheGluPhePheIleGlnAsnAspGlnCysGlnGluMet

406 GACACCACCACTGACAAGTGGGTAAAACTTACAGACAATGGAGAA
    AspThrThrThrAspLysTrpValLysLeuThrAspAsnGlyGlu

451 TGGGGCTCTCATTCTGTAATGCTGAAATCAGGCACAAACATACTC
    TrpGlySerHisSerValMetLeuLysSerGlyThrAsnIleLeu

496 TACTGGAGAACTACAGGCATCCTTATGGGTTCTAAGGCGGTCAAG
    TyrTrpArgThrThrGlyIleLeuMetGlySerLysAlaValLys

541 CCTGTGCTGGTAAAAAATATCACAATTGAAGGGGTGGCGTACACA
    ProValLeuValLysAsnIleThrIleGluGlyValAlaTyrThr

586 TCAGAATGTTTTCCTTGCAAGCCAGGCACATTCAGCAACAAACCA
    SerGluCysPheProCysLysProGlyThrPheSerAsnLysPro

631 GGTTCATTCAACTGCCAGGTGTGTCCCAGAAACACCTATTCTGAG
    GlySerPheAsnCysGlnValCysProArgAsnThrTyrSerGlu

676 AAAGGAGCCAAAGAATGTATAAGGTGTAAAGACGACTCTCAATTT
    LysGlyAlaLysGluCysIleArgCysLysAspAspSerGlnPhe

721 TCAGAGGAAGGATCCAGTGAGTGTACAGAGCGCCCTCCCTGTACC
    SerGluGluGlySerSerGluCysThrGluArgProProCysThr

766 ACAAAAGACTATTTCCAGATCCATACTCCATGTGATGAAGAAGGA
    ThrLysAspTyrPheGlnIleHisThrProCysAspGluGluGly

811 AAGACACAGATAATGTACAAGTGGATAGAGCCCAAAATCTGCCGG
    LysThrGlnIleMetTyrLysTrpIleGluProLysIleCysArg

856 GAGGATCTCACAGATGCTATTAGATTGCCCCCTTCTGGAGAGAAG
    GluAspLeuThrAspAlaIleArgLeuProProSerGlyGluLys

901 AAGGATTGTCCGCCTTGCAACCCTGGATTTTATAACAATGGATCA
    LysAspCysProProCysAsnProGlyPheTyrAsnAsnGlySer

946 TCTTCTTGCCATCCCTGTCCTCCTGGAACATTTTCAGATGGAACC
    S rSerCysHisProCysProProGlyThrPheS rAspGlyThr
```

Fig. 5

991 AAAGAATGTAGACCATGTCCAGCAGGAACGGAGCCTGCACTTGGC
LysGluCysArgProCysProAlaGlyThrGluProAlaLeuGly

1036 TTTGAATATAAATGGTGGAATGTCCTTCCTGGCAACATGAAAACT
PheGluTyrLysTrpTrpAsnValLeuProGlyAsnMetLysThr

1081 TCCTGCTTCAATGTTGGGAATTCAAAGTGCGATGGAATGAATGGT
SerCysPheAsnValGlyAsnSerLysCysAspGlyMetAsnGly

1126 TGGGAGGTGGCTGGAGATCATATCCAGAGTGGGGCTGGAGGTTCT
TrpGluValAlaGlyAspHisIleGlnSerGlyAlaGlyGlySer

1171 GACAATGATTACCTGATCTTAAACTTGCATATCCCAGGATTTAAA
AspAsnAspTyrLeuIleLeuAsnLeuHisIleProGlyPheLys

1216 CCACCAACATCTATGACTGGAGCCACGGGTTCTGAACTAGGAAGA
ProProThrSerMetThrGlyAlaThrGlySerGluLeuGlyArg

1261 ATAACATTTGTCTTTGAGACCCTCTGTTCAGCTGACTGTGTTTTG
IleThrPheValPheGluThrLeuCysSerAlaAspCysvalLeu

1306 TACTTCATGGTGGATATTAATAGAAAAAGTACAAATGTGGTAGAA
TyrPheMetValAspIleAsnArgLysSerThrAsnValValGlu

1351 TCGTGGGGTGGAACCAAAGAAAAACAAGCTTACACCCATATCATC
SerTrpGlyGlyThrLysGluLysGlnAlaTyrThrHisIleIle

1396 TTCAAGAATGCAACTTTTACATTTACATGGGGCATTCCCAGAGAA
PheLysAsnAlaThrPheThrPheThrTrpGlyIleProArgGlu

1441 CTAATTCAGGGTCCAAGATAATAGACGGTTCCNCCATTGACATGT
LeuIleGlnGlyProArg

1486 TTGAAGGATTTATTCCTATTCAC

Fig. 5 Continued

```
  1 CGGCCCTTCTCACACTCCTGCCCTGCTGATGTGGAACGGGGTTTG
 46 GGGTTCTGCAGGGCTATTGTCTGCGCTGGGGAAGGGGACAGGCCG
 91 GGACCGGGACCTCCGCTCGCAGCCGGCCGCACCAGCAGGACAGCT

136 GGCCTGAAGCTCAGAGCCGGGGCGTGCGCCATGGCCCCACACTGG
                                  MetAlaProHisTrp

181 GCTGTCTGGCTGCTGGCAGCAAGGCTGTGGGGCCTGGGCATTGGG
    AlaValTrpLeuLeuAlaAlaArgLeuTrpGlyLeuGlyIleGly

226 GCTGAGGTGTGGTGGAACCTTGTGCCGCGTAAGACAGTGTCTTCT
    AlaGluValTrpTrpAsnLeuValProArgLysThrValSerSer

271 GGGGAGCTGGCCACGGTAGTACGGCGGTTCTCCCAGACCGGCATC
    GlyGluLeuAlaThrValValArgArgPheSerGlnThrGlyIle

316 CAGGACTTCCTGACACTGACGCTGACGGAGCCCACTGGGCTTCTG
    GlnAspPheLeuThrLeuThrLeuThrGluProThrGlyLeuLeu

361 TACGTGGGCGCCCGAGAGGCCCTGTTTGCCTTCAGCATGGAGGCC
    TyrValGlyAlaArgGluAlaLeuPheAlaPheSerMetGluAla

406 CTGGAGCTGCAAGGAGCGATCTCCTGGGAGGCCCCCGTGGAGAAG
    LeuGluLeuGlnGlyAlaIleSerTrpGluAlaProValGluLys

451 AAGACTGAGTGTATCCAGAAAGGGAAGAACAACCAGACCGAGTGC
    LysThrGluCysIleGlnLysGlyLysAsnAsnGlnThrGluCys

496 TTCAACTTCATCCGCTTCCTGCAGCCCTACAATGCCTCCCACCTG
    PheAsnPheIleArgPheLeuGlnProTyrAsnAlaSerHisLeu

541 TACGTCTGTGGCACCTACGCCTTCCAGCCCAAGTGCACCTACGTC
    TyrValCysGlyThrTyrAlaPheGlnProLysCysThrTyrVal

586 AACATGCTCACCTTCACTTTGGAGCATGGAGAGTTTGAAGATGGG
    AsnMetLeuThrPheThrLeuGluHisGlyGluPheGluAspGly

631 AAGGGCAAGTGTCCCTATGACCCAGCTAAGGGCCATGCTGGCCTT
    LysGlyLysCysProTyrAspProAlaLysGlyHisAlaGlyLeu

676 CTTGTGGATGGTGAGCTGTACTCGGCCACACTCAACAACTTCCTG
    LeuValAspGlyGluLeuTyrSerAlaThrLeuAsnAsnPheLeu

721 GGCACGGAACCCATTATCCTGCGTAACATGGGGCCCCACCACTCC
    GlyThrGluProIleIleLeuArgAsnMetGlyProHisHisSer

766 ATGAAGACAGAGTACCTGGCCTTTTGGCTCAACGAACCTCACTTT
    MetLysThrGluTyrLeuAlaPheTrpLeuAsnGluProHisPhe

811 GTAGGCTCTGCCTATGTACCTGAGAGTGTGGGCAGCTTCACGGGG
    ValGlySerAlaTyrValProGluSerValGlySerPheThrGly

856 GACGACGACAAGGTCTACTTCTTCTTCAGGGAGCGGGCAGTGGAG
    AspAspAspLysValTyrPhePhePheArgGluArgAlaValGlu
```

Fig. 6

901 TCCGACTGCTATGCCGAGCAGGTGGTGGCTCGTGTGGCCCGTGTC
SerAspCysTyrAlaGluGlnValValAlaArgValAlaArgVal

946 TGCAAGGGCGATATGGGGGGCGCACGGACCCTGCAGAGGAAGTGG
CysLysGlyAspMetGlyGlyAlaArgThrLeuGlnArgLysTrp

991 ACCACGTTCCTGAAGGCGCGGCTGGCATGCTCTGCCCCGAACTGG
ThrThrPheLeuLysAlaArgLeuAlaCysSerAlaProAsnTrp

1036 CAGCTCTACTTCAACCAGCTGCAGGCGATGCACACCCTGCAGGAC
GlnLeuTyrPheAsnGlnLeuGlnAlaMetHisThrLeuGlnAsp

1081 ACCTCCTGGCACAACACCACCTTCTTTGGGGTTTTTCAAGCACAG
ThrSerTrpHisAsnThrThrPhePheGlyValPheGlnAlaGln

1126 TGGGGTGACATGTACCTGTCGGCCATCTGTGAGTACCAGTTGGAA
TrpGlyAspMetTyrLeuSerAlaIleCysGluTyrGlnLeuGlu

1171 GAGATCCAGCGGGTGTTTGAGGGCCCCTATAAGGAGTACCATGAG
GluIleGlnArgValPheGluGlyProTyrLysGluTyrHisGlu

1216 GAAGCCCAGAAGTGGGACCGCTACACTGACCCTGTACCCAGCCCT
GluAlaGlnLysTrpAspArgTyrThrAspProValProSerPro

1261 CGGCCTGGCTCGTGCATTAACAACTGGCATCGGCGCCACGGCTAC
ArgProGlySerCysIleAsnAsnTrpHisArgArgHisGlyTyr

1306 ACCAGCTCCCTGGAGCTACCCGACAACATCCTCAACTTCGTCAAG
ThrSerSerLeuGluLeuProAspAsnIleLeuAsnPheValLys

1351 AAGCACCCGCTGATGGAGGAGCAGGTGGGGCCTCGGTGGAGCCGC
LysHisProLeuMetGluGluGlnValGlyProArgTrpSerArg

1396 CCCCTGCTCGTGAAGAAGGGCACCAACTTCACCCACCTGGTGGCC
ProLeuLeuValLysLysGlyThrAsnPheThrHisLeuValAla

1441 GACCGGGTTACAGGACTTGATGGAGCCACCTATACAGTGCTGTTC
AspArgValThrGlyLeuAspGlyAlaThrTyrThrValLeuPhe

1486 ATTGGCACAGGAGACGGCTGGCTGCTCAAGGCTGTGAGCCTGGGG
IleGlyThrGlyAspGlyTrpLeuLeuLysAlaValSerLeuGly

1531 CCCTGGGTTCACCTGATTGAGGAGCTGCAGCTGTTTGACCAGGAG
ProTrpValHisLeuIleGluGluLeuGlnLeuPheAspGlnGlu

1576 CCCATGAGAAGCCTGGTGCTATCTCAGAGCAAGAAGCTGCTCTTT
ProMetArgSerLeuValLeuSerGlnSerLysLysLeuLeuPhe

1621 GCCGGCTCCCGCTCTCAGCTGGTGCAGCTGCCCGTGGCCGACTGC
AlaGlySerArgSerGlnLeuValGlnLeuProValAlaAspCys

1666 ATAAAGTATCGCTCCTGTGCAGACTGTGTCCTCGCCCGGGACCCC
IleLysTyrArgSerCysAlaAspCysValLeuAlaArgAspPro

Fig. 6 Continued

1711 TATTGCGCCTGGAGCGTCAACACCAGCCGCTGTGTGGCCGTGGGT
TyrCysAlaTrpSerValAsnThrSerArgCysValAlaValGly

1756 GGCCACTTTGGATCTTTACTGATCCAGCATGTGATGACCTCGGAC
GlyHisPheGlySerLeuLeuIleGlnHisValMetThrSerAsp

1801 ACTTCAGGCATTTGCAACCTCCGTGGCAGTAAGAAAGTCAGGCCC
ThrSerGlyIleCysAsnLeuArgGlySerLysLysValArgPro

1846 ACTCCCAAAAACATCACGGTGGTGGCGGGCACAGACCTGGTGCTG
ThrProLysAsnIleThrValValAlaGlyThrAspLeuValLeu

1891 CCCTGCCACCTCTCCTCCACTTGGCCCCGGGGTTCAGTGGTATTT
ProCysHisLeuSerSerThrTrpProArgGlySerValValPhe

1936 TAAACTTGCCTTCTTCCTGTACAGGGCTGGGAAAGGCTGTGTTAG
1981 GGGAAAAAAAGGAAAGGGTGGGCCTGCTGTGGACAATGGCATACT
2026 CTCTTCCAGCCCTAGGAGGAGGGCTCCTAACAGTGTAACTTATTG
2071 TGTCCCCGCGTATTTATTTGTTGTAAATATTTGAGTATTTTTATA
2116 TTGACAAATAAAATGGAGAAAATGAAAAAAAAAAAAAAAA

Fig. 6 Continued

```
  1 CGGCCCTTCTCACACTCCTGCCCTGCTGATGTGGAACGGGGTTTG
 46 GGGTTCTGCAGGGCTATTGTCTGCGCTGGGGAAGGGGACAGGCCG
 91 GGACCGGGACCTCCGCTCGCAGCCGGCCGCACCAGCAGGACAGCT

136 GGCCTGAAGCTCAGAGCCGGGGCGTGCGCCATGGCCCCACACTGG
                                   MetAlaProHisTrp

181 GCTGTCTGGCTGCTGGCAGCAAGGCTGTGGGGCCTGGGCATTGGG
    AlaValTrpLeuLeuAlaAlaArgLeuTrpGlyLeuGlyIleGly

226 GCTGAGGTGTGGTGGAACCTTGTGCCGCGTAAGACAGTGTCTTCT
    AlaGluValTrpTrpAsnLeuValProArgLysThrValSerSer

271 GGGGAGCTGGCCACGGTAGTACGGCGGTTCTCCCAGACCGGCATC
    GlyGluLeuAlaThrValValArgArgPheSerGlnThrGlyIle

316 CAGGACTTCCTGACACTGACGCTGACGGAGCCCACTGGGCTTCTG
    GlnAspPheLeuThrLeuThrLeuThrGluProThrGlyLeuLeu

361 TACGTGGGCGCCCGAGAGGCCCTGTTTGCCTTCAGCATGGAGGCC
    TyrValGlyAlaArgGluAlaLeuPheAlaPheSerMetGluAla

406 CTGGAGCTGCAAGGAGCGATCTCCTGGGAGGCCCCCGTGGAGAAG
    LeuGluLeuGlnGlyAlaIleSerTrpGluAlaProValGluLys

451 AAGACTGAGTGTATCCAGAAAGGGAAGAACAACCAGACCGAGTGC
    LysThrGluCysIleGlnLysGlyLysAsnAsnGlnThrGluCys

496 TTCAACTTCATCCGCTTCCTGCAGCCCTACAATGCCTCCCACCTG
    PheAsnPheIleArgPheLeuGlnProTyrAsnAlaSerHisLeu

541 TACGTCTGTGGCACCTACGCCTTCCAGCCCAAGTGCACCTACGTC
    TyrValCysGlyThrTyrAlaPheGlnProLysCysThrTyrVal

586 AACATGCTCACCTTCACTTTGGAGCATGGAGAGTTTGAAGATGGG
    AsnMetLeuThrPheThrLeuGluHisGlyGluPheGluAspGly

631 AAGGGCAAGTGTCCCTATGACCCAGCTAAGGGCCATGCTGGCCTT
    LysGlyLysCysProTyrAspProAlaLysGlyHisAlaGlyLeu

676 CTTGTGGATGGTGAGCTGTACTCGGCCACACTCAACAACTTCCTG
    LeuValAspGlyGluLeuTyrSerAlaThrLeuAsnAsnPheLeu

721 GGCACGGAACCCATTATCCTGCGTAACATGGGGCCCCACCACTCC
    GlyThrGluProIleIleLeuArgAsnMetGlyProHisHisSer

766 ATGAAGACAGAGTACCTGGCCTTTTGGCTCAACGAACCTCACTTT
    MetLysThrGluTyrLeuAlaPheTrpLeuAsnGluProHisPhe

811 GTAGGCTCTGCCTATGTACCTGAGAGTGTGGGCAGCTTCACGGGG
    ValGlySerAlaTyrValProGluSerValGlySerPheThrGly

856 GACGACGACAAGGTCTACTTCTTCTTCAGGGAGCGGGCAGTGGAG
    AspAspAspLysValTyrPhePhePheArgGluArgAlaValGlu
```

Fig. 7

```
901  TCCGACTGCTATGCCGAGCAGGTGGTGGCTCGTGTGGCCCGTGTC
     SerAspCysTyrAlaGluGlnValValAlaArgValAlaArgVal

946  TGCAAGGGCGATATGGGGGCGCACGGACCCTGCAGAGGAAGTGG
     CysLysGlyAspMetGlyGlyAlaArgThrLeuGlnArgLysTrp

991  ACCACGTTCCTGAAGGCGCGGCTGGCATGCTCTGCCCCGAACTGG
     ThrThrPheLeuLysAlaArgLeuAlaCysSerAlaProAsnTrp

1036 CAGCTCTACTTCAACCAGCTGCAGGCGATGCACACCCTGCAGGAC
     GlnLeuTyrPheAsnGlnLeuGlnAlaMetHisThrLeuGlnAsp

1081 ACCTCCTGGCACAACACCACCTTCTTTGGGGTTTTTCAAGCACAG
     ThrSerTrpHisAsnThrThrPhePheGlyValPheGlnAlaGln

1126 TGGGGTGACATGTACCTGTCGGCCATCTGTGAGTACCAGTTGGAA
     TrpGlyAspMetTyrLeuSerAlaIleCysGluTyrGlnLeuGlu

1171 GAGATCCAGCGGGTGTTTGAGGGCCCCTATAAGGAGTACCATGAG
     GluIleGlnArgValPheGluGlyProTyrLysGluTyrHisGlu

1216 GAAGCCCAGAAGTGGGACCGCTACACTGACCCTGTACCCAGCCCT
     GluAlaGlnLysTrpAspArgTyrThrAspProValProSerPro

1261 CGGCCTGGCTCGTGCATTAACAACTGGCATCGGCGCCACGGCTAC
     ArgProGlySerCysIleAsnAsnTrpHisArgArgHisGlyTyr

1306 ACCAGCTCCCTGGAGCTACCCGACAACATCCTCAACTTCGTCAAG
     ThrSerSerLeuGluLeuProAspAsnIleLeuAsnPheValLys

1351 AAGCACCCGCTGATGGAGGAGCAGGTGGGGCCTCGGTGGAGCCGC
     LysHisProLeuMetGluGluGlnValGlyProArgTrpSerArg

1396 CCCCTGCTCGTGAAGAAGGGCACCAACTTCACCCACCTGGTGGCC
     ProLeuLeuValLysLysGlyThrAsnPheThrHisLeuValAla

1441 GACCGGGTTACAGGACTTGATGGAGCCACCTATACAGTGCTGTTC
     AspArgValThrGlyLeuAspGlyAlaThrTyrThrValLeuPhe

1486 ATTGGCACAGGAGACGGCTGGCTGCTCAAGGCTGTGAGCCTGGGG
     IleGlyThrGlyAspGlyTrpLeuLeuLysAlaValSerLeuGly

1531 CCCTGGGTTCACCTGATTGAGGAGCTGCAGCTGTTTGACCAGGAG
     ProTrpValHisLeuIleGluGluLeuGlnLeuPheAspGlnGlu

1576 CCCATGAGAAGCCTGGTGCTATCTCAGAGCAAGAAGCTGCTCTTT
     ProMetArgSerLeuValLeuSerGlnSerLysLysLeuLeuPhe

1621 GCCGGCTCCCGCTCTCAGCTGGTGCAGCTGCCCGTGGCCGACTGC
     AlaGlySerArgSerGlnLeuValGlnLeuProValAlaAspCys

1666 ATAAAGTATCGCTCCTGTGCAGACTGTGTCCTCGCCCGGGACCCC
     IleLysTyrArgSerCysAlaAspCysValLeuAlaArgAspPro
```

Fig. 7 Continued

1711 TATTGCGCCTGGAGCGTCAACACCAGCCGCTGTGTGGCCGTGGGT
TyrCysAlaTrpSerValAsnThrSerArgCysValAlaValGly

1756 GGCCACTTTGGATCTTTACTGATCCAGCATGTGATGACCTCGGAC
GlyHisPheGlySerLeuLeuIleGlnHisValMetThrSerAsp

1801 ACTTCAGGCATTTGCAACCTCCGTGGCAGTAAGATACAGTCAGGC
ThrSerGlyIleCysAsnLeuArgGlySerLysIleGlnSerGly

1846 CCACTNCCCAAAAACATCACGGTGGTGGCGGGCACAGACCTGGTG
ProLeuProLysAsnIleThrValValAlaGlyThrAspLeuVal

1891 CTGCCCTGCCACCTCTCCTCCAACTTGGCCCTGCCCGACTCCAAC
LeuProCysHisLeuSerSerAsnLeuAlaLeuProAspSerAsn

1936 CCCGAGGAGTCATCAGTATGAGGGGAACCCCCACCGCGTCGGCGG
ProGluGluSerSerVal

1981 ANAGCGTGGGAGGTGTAGCTCCTACTTTTGCACAGGCACCAGCTA
2026 TCTCAGGGACATGGCACGGGCACCTGCTCTGTCTGGGACAGATAC
2071 TGCCCAGCACCCACCCGGCCATGAGGACCTGCTCTGCTCAGCACG
2116 GGCACTGCACTTGGTGTGGTCACCAGGGCACCAGCTCGCAGAAGG
2161 CATCTTCCTCCTCTCTGTGAATCACAGACACGCGGGACCCCAGCC
2206 GCCAAAATTTTCAAGGCAGAAGTTNAAGATGTGTGTTTGNTGTAT
2251 TTGACATGTGTTTGTGTGTGTGTGTATGTGTGTG

Fig. 7 Continued

```
  1 ACCGACGTCGAATATCCATGCATCCGCGTGCAGGTGGCAGACGGA
 46 CTCCGGCGGAATGGGGGGTGTGGCTGCTCCGCCAGGGTCCCCAGG
 91 GTGGGAGAGCGGCTCCGCGGCCACCGATGCCCGGACCCCCTCTGT

136 CTTCTGCTAGACATGCTCTTCCTCTCGTTTCATGCAGGCTCTTGG
                MetLeuPheLeuSerPheHisAlaGlySerTrp

181 GAAAGCTGGTGCTGCTGCTGCCTGATTCCCGCCGACAGACCTTGG
    GluSerTrpCysCysCysCysLeuIleProAlaAspArgProTrp

226 GACCGGGGCCAACACTGGCAGCTGGAGATGGCGGACACGAGATCC
    AspArgGlyGlnHisTrpGlnLeuGluMetAlaAspThrArgSer

271 GTGCACGAGACTAGGTTTGAGGCGGCCGTGAAGGTGATCCAGAGT
    ValHisGluThrArgPheGluAlaAlaValLysValIleGlnSer

316 TTGCCGAAGAATGGTTCATTCCAGCCAACAAATGAAATGATGCTT
    LeuProLysAsnGlySerPheGlnProThrAsnGluMetMetLeu

361 AAATTTTATAGCTTCTATAAGCAGGCAACTGAAGGACCCTGTAAA
    LysPheTyrSerPheTyrLysGlnAlaThrGluGlyProCysLys

406 CTTTCAAGGCCTGGATTTTGGGATCCTATTGGAAGATATAAATGG
    LeuSerArgProGlyPheTrpAspProIleGlyArgTyrLysTrp

451 GATGCTTGGAGTTCACTGGGTGATATGACCAAAGAGGAAGCCATG
    AspAlaTrpSerSerLeuGlyAspMetThrLysGluGluAlaMet

496 ATTGCATATGTTGAAGAAATGAAAAAGATTATTGAAACTATGCCA
    IleAlaTyrValGluGluMetLysLysIleIleGluThrMetPro

541 ATGACTGAGAAAGTTGAAGAATTGCTGCGTGTCATAGGTCCATTT
    MetThrGluLysValGluGluLeuLeuArgValIleGlyProPhe

586 TATGAAATTGTCGAGGACAAAAAGAGTGGCAGGAGTTCTGATATA
    TyrGluIleValGluAspLysLysSerGlyArgSerSerAspIle

631 ACCTCAGTCCGACTGGAGAAAATCTCTAAATGTTTAGAAGATCTT
    ThrSerValArgLeuGluLysIleSerLysCysLeuGluAspLeu

676 GGTAATGTTCTCACTTCTACTCCAAACGCCAAAACCGTTAATGGT
    GlyAsnValLeuThrSerThrProAsnAlaLysThrValAsnGly

721 AAAGCTGAAAGCAGTGACAGTGGAGCCGAGTCTGAGGAAGAAGAG
    LysAlaGluSerSerAspSerGlyAlaGluSerGluGluGluGlu

766 GCCCAAGAAGAAGTGAAAGGAGCAGAACAAAGTGATAATGATAAG
    AlaGlnGluGluValLysGlyAlaGluGlnSerAspAsnAspLys

811 AAAATGATGAAGAAGTCAGCAGACCATAAGAATTTGGAAGTCATT
    LysMetMetLysLysSerAlaAspHisLysAsnLeuGluValIle
```

Fig. 8

856 GTCACTAATGGCTATGATAAAGATGGCTTTGTTCAGGATATACAG
ValThrAsnGlyTyrAspLysAspGlyPheValGlnAspIleGln

901 AATGACATTCATGCCAGTTCTTCCCTGAATGGCAGAAGCACTGAA
AsnAspIleHisAlaSerSerSerLeuAsnGlyArgSerThrGlu

946 GAAGTAAAGCCCATTGATGAAAACTTGGGGCAAACTGGAAAATCT
GluValLysProIleAspGluAsnLeuGlyGlnThrGlyLysSer

991 GCTGTTTGCATTCACCAAGATATAAATGATGATCATGTTGAAGAT
AlaValCysIleHisGlnAspIleAsnAspAspHisValGluAsp

1036 GTTACAGGAATTCAGCATTTGACAAGCGATTCAGACAGTGAAGTT
ValThrGlyIleGlnHisLeuThrSerAspSerAspSerGluVal

1081 TACTGTGATTCTATGGAACAATTTGGACAAGAAGAGTCTTTAGAC
TyrCysAspSerMetGluGlnPheGlyGlnGluGluSerLeuAsp

1126 AGCTTTACGTCCAACAATGGACCATTTCAGTATTACTTGGGTGGT
SerPheThrSerAsnAsnGlyProPheGlnTyrTyrLeuGlyGly

1171 CATTCCAGTCAACCCATGGAAAATTCTGGATTTCGTGAAGATATT
HisSerSerGlnProMetGluAsnSerGlyPheArgGluAspIle

1216 CAAGTACCTCCTGGAAATGGCAACATTGGGAATATGCAGGTGGTT
GlnValProProGlyAsnGlyAsnIleGlyAsnMetGlnValVal

1261 GCAGTTGAAGGAAAAGGTGAAGTCAAGCATGGAGGAGAAGATGGC
AlaValGluGlyLysGlyGluValLysHisGlyGlyGluAspGly

1306 AGGAATAACAGCGGAGCACCACACCGGGAGAAGCGAGGCGGAGAA
ArgAsnAsnSerGlyAlaProHisArgGluLysArgGlyGlyGlu

1351 ACTGACGAATTCTCTAATGTTAGAAGAGGAAGAGGACATAGGATG
ThrAspGluPheSerAsnValArgArgGlyArgGlyHisArgMet

1396 CAACACTTGAGCGAAGGAACCAAGGGCCGGCAGGTGGGAAGTGGA
GlnHisLeuSerGluGlyThrLysGlyArgGlnValGlySerGly

1441 GGTGATGGGGAGCGCTGGGGCTCCGACAGAGGGTCCCGAGGCAGC
GlyAspGlyGluArgTrpGlySerAspArgGlySerArgGlySer

1486 CTCAATGAGCAGATCGCCCTCGTGCTGATGAGACTGCAGGAGGAC
LeuAsnGluGlnIleAlaLeuValLeuMetArgLeuGlnGluAsp

1531 ATGCAGAATGTCCTTCAGAGACTGCAGAAACTGGAAATGCTGACT
MetGlnAsnValLeuGlnArgLeuGlnLysLeuGluMetLeuThr

1576 GCTTTGCAGGCAAAATCATCAACATCAACATTGCAGACTGCTCCT
AlaLeuGlnAlaLysSerSerThrSerThrLeuGlnThrAlaPro

1621 CAGCCCACCTCACAGAGACCATCTTGGTGGCCCTTCGAGATGTCT
GlnProThrS rGlnArgProSerTrpTrpProPheGluMetS r

Fig. 8 Continued

1666 CCTGGTGTGCTAACGTTTGCCATCATATGGCCTTTTATTGCACAG
ProGlyValLeuThrPheAlaIleIleTrpProPheIleAlaGln

1711 TGGTTGGTGTATTTATACTATCAAAGAAGGAGAAGAAAACTGAAC
TrpLeuValTyrLeuTyrTyrGlnArgArgArgArgLysLeuAsn

1756 TGAGGGAAAATGGTGTTTTCCTCAAGAAGACTACTGGAACTGGAT
1801 GACCTCAGAATGAACTGGATTGTGGTGTTCACAAGAAAATCTTAG
1849 TTTGTGATGATTACATTGCTTTTTGTTGTCCNGTAGTTTAGTTTG
1891 TGTACATATATACACATATATATTTTGCACTACACAAACG

Fig. 8 Continued

```
  1 CATTCTAGCTGCCTGCTGCCTCCGCAGCGTCCCCCCAGCTCTCCC
 46 TGTGCTAACTGCCTGCACCTTGGACAGAGCGGGTGCGCAAATCAG

 91 AAGGATTAGTTGGGACCTGCCTTGGCGACCCCATGGCATCCCCCA
                                     MetAlaSerProA

136 GAACCGTAACTATTGTGGCCCTCTCAGTGGCCCTGGGACTCTTCT
    rgThrValThrIleValAlaLeuSerValAlaLeuGlyLeuPheP

181 TTGTTTTCATGGGGACTATCAAGCTGACCCCCAGGCTCAGCAAGG
    heValPheMetGlyThrIleLysLeuThrProArgLeuSerLysA

226 ATGCCTACAGTGAGATGAAACGTGCTTACAAGAGCTATGTTCGAG
    spAlaTyrSerGluMetLysArgAlaTyrLysSerTyrValArgA

271 CCCTCCCTCTGCTGAAGAAAATGGGGATCAATTCCATTCTCCTCC
    laLeuProLeuLeuLysLysMetGlyIleAsnSerIleLeuLeuA

316 GAAAAAGCATTGGTGCCCTTGAAGTGGCCTGTGGCATCGTCATGA
    rgLysSerIleGlyAlaLeuGluValAlaCysGlyIleValMetT

361 CCCTTGTGCCTGGGCGTCCCAAAGATGTGGCCAACTTCTTCCTAC
    hrLeuValProGlyArgProLysAspValAlaAsnPhePheLeuL

406 TGTTGCTGGTGTTGGCTGTGCTCTTCTTCCACCAGCTGGTCGGTG
    euLeuLeuValLeuAlaValLeuPhePheHisGlnLeuValGlyA

451 ATCCTCTCAAACGCTACGCCCATGCTCTGGTGTTTGGAATCCTGC
    spProLeuLysArgTyrAlaHisAlaLeuValPheGlyIleLeuL

496 TCACTTGCCGCCTGCTGATTGCTCGCAAGCCCGAAGACCGGTCTT
    euThrCysArgLeuLeuIleAlaArgLysProGluAspArgSerS

541 CTGAGAAGAAGCCTTTGCCAGGGAATGCTGAGGAGCAACCCTCCT
    erGluLysLysProLeuProGlyAsnAlaGluGluGlnProSerL

586 TATATGAGAAGGCCCCTCAGGGCAAAGTGAAGGTGTCATAGAAAA
    euTyrGluLysAlaProGlnGlyLysValLysValSer
```

Fig. 9

```
  1 TGCGCCCTCTGTCTGGCACTCCCTAGTGAGATGAACCCGGTACCT
 46 CAGATGGAAATGCAGAAATCACCCGTCTTCTGCGTCGCTCACGCT
 91 GGGAGCTGTAGACCAGAGCTGTTCCTATTCGGCCATCTTGGCTCC
136 TCCCTCGAAAGATTATCACTTTGAATATACGGAATGTGATAGCAG
181 TGGCTCCAGGTGGAGAGTTGCCATTCCAAATTCTGCAGTGGACTG
226 CTCTGGCCTGCCTGACCCAGTGAGAGGCAAAGAATGCACTTTCTC

271 CTGTGCTTCTGGAGAGTATCTAGAAATGAAGAACCAGGTATGCAG
                                MetLysAsnGlnValCysSe

316 TAAGTGTGGTGAAGGCACCTATTCCTTGGGCAGTGGCATCAAATT
    rLysCysGlyGluGlyThrTyrSerLeuGlySerGlyIleLysPh

361 TGATGAATGGGATGAATTGCCGGCAGGATTTTCTAACATCGCAAC
    eAspGluTrpAspGluLeuProAlaGlyPheSerAsnIleAlaTh

406 ATTCATGGACACTGTGGTGGGCCCTTCTGACAGCAGGCCAGACGG
    rPheMetAspThrValValGlyProSerAspSerArgProAspGl

451 CTGTAACAACTCTTCTTGGATCCCTCGTGGAAACTACATAGAATC
    yCysAsnAsnSerSerTrpIleProArgGlyAsnTyrIleGluSe

496 TAATCGTGATGACTGCACGGTGTCTTTGATCTATGCTGTGCACCT
    rAsnArgAspAspCysThrValSerLeuIleTyrAlaValHisLe

541 TAAGAAGTCAGGCTATGTCTTCTTTGAGTACCAGTATGTCGACAA
    uLysLysSerGlyTyrValPhePheGluTyrGlnTyrValAspAs

586 CAACATCTTCTTTGAGTTCTTTATTCAAAATGATCAGTGCCAGGA
    nAsnIlePhePheGluPhePheIleGlnAsnAspGlnCysGlnGl

631 GATGGACACCACCACTGACAAGTGGGTAAAACTTACAGACAATGG
    uMetAspThrThrThrAspLysTrpValLysLeuThrAspAsnGl

676 AGAATGGGGCTCTCATTCTGTAATGCTGAAATCAGGCACAAACAT
    yGluTrpGlySerHisSerValMetLeuLysSerGlyThrAsnIl

721 ACTCTACTGGAGAACTACAGGCATCCTTATGGGTTCTAAGGCGGT
    eLeuTyrTrpArgThrThrGlyIleLeuMetGlySerLysAlaVa

766 CAAGCCTGTGCTGGTAAAAAATATCACAATTGAAGGGGTGGCGTA
    lLysProValLeuValLysAsnIleThrIleGluGlyValAlaTy

811 CACATCAGAATGTTTTCCTTGCAAGCCAGGCACATTCAGCAACAA
    rThrSerGluCysPheProCysLysProGlyThrPheSerAsnLy

856 ACCAGGTTCATTCAACTGCCAGGTGTGTCCCAGAAACACCTATTC
    sProGlySerPheAsnCysGlnValCysProArgAsnThrTyrSe

901 TGAGAAAGGAGCCAAAGAATGTATAAGGTGTAAAGACGACTCTCA
    rGluLysGlyAlaLysGluCysIleArgCysLysAspAspSerGl

946 ATTTTCAGAGGAAGGATCCAGTGAGTGTACAGAGCGCCCTCCCTG
    nPheSerGluGluGlySerSerGluCysThrGluArgProProCy
```

Fig. 10

991 TACCACAAAAGACTATTTCCAGATCCATACTCCATGTGATGAAGA
sThrThrLysAspTyrPheGlnIleHisThrProCysAspGluGl

1036 AGGAAAGACACAGATAATGTACAAGTGGATAGAGCCCAAAATCTG
uGlyLysThrGlnIleMetTyrLysTrpIleGluProLysIleCy

1081 CCGGGAGGATCTCACAGATGCTATTAGATTGCCCCCTTCTGGAGA
sArgGluAspLeuThrAspAlaIleArgLeuProProSerGlyGl

1126 GAAGAAGGATTGTCCGCCTTGCAACCCTGGATTTTATAACAATGG
uLysLysAspCysProProCysAsnProGlyPheTyrAsnAsnGl

1171 ATCATCTTCTTGCCATCCCTGTCCTCCTGGAACATTTTCAGATGG
ySerSerSerCysHisProCysProProGlyThrPheSerAspGl

1216 AACCAAAGAATGTAGACCATGTCCAGCAGGAACGGAGCCTGCACT
yThrLysGluCysArgProCysProAlaGlyThrGluProAlaLe

1261 TGGCTTTGAATATAAATGGTGGAATGTCCTTCCTGGCAACATGAA
uGlyPheGluTyrLysTrpTrpAsnValLeuProGlyAsnMetLy

1306 AACTTCCTGCTTCAATGTTGGGAATTCAAAGTGCGATGGAATGAA
sThrSerCysPheAsnValGlyAsnSerLysCysAspGlyMetAs

1351 TGGTTGGGAGGTGGCTGGAGATCATATCCAGAGTGGGGCTGGAGG
nGlyTrpGluValAlaGlyAspHisIleGlnSerGlyAlaGlyGl

1396 TTCTGACAATGATTACCTGATCTTAAACTTGCATATCCCAGGATT
ySerAspAsnAspTyrLeuIleLeuAsnLeuHisIleProGlyPh

1441 TAAACCACCAACATCTATGACTGGAGCCACGGGTTCTGAACTAGG
eLysProProThrSerMetThrGlyAlaThrGlySerGluLeuGl

1486 AAGAATAACATTTGTCTTTGAGACCCTCTGTTCAGCTGACTGTGT
yArgIleThrPheValPheGluThrLeuCysSerAlaAspCysVa

1531 TTTGTACTTCATGGTGGATATTAATAGAAAAAGTACAAATGTGGT
lLeuTyrPheMetValAspIleAsnArgLysSerThrAsnValVa

1576 AGAATCGTGGGGTGGAACCAAAGAAAAACAAGCTTACACCCATAT
lGluSerTrpGlyGlyThrLysGluLysGlnAlaTyrThrHisIl

1621 CATCTTCAAGAATGCAACTTTTACATTTACATGGGGCATTCCCAG
eIlePheLysAsnAlaThrPheThrPheThrTrpGlyIleProAr

1666 AGAACTAATTCAGGGTCCAAGATAATAGACGGTTCCNCCATTGAC
gGluLeuIleGlnGlyProArg

1711 ATGTTTGAAGGATTTATTCCTATTCAC

Fig. 10 Continued

1 CGGCCCTTCTCACACTCCTGCCCTGCTGATGTGGAACGGGGTTTG
46 GGGTTCTGCAGGGCTATTGTCTGCGCTGGGGAAGGGGACAGGCCG
91 GGACCGGGACCTCCGCTCGCAGCCGGCCGCACCAGCAGGACAGCT

136 GGCCTGAAGCTCAGAGCCGGGGCGTGCGCCATGGCCCCACACTGG
MetAlaProHisTrp

181 GCTGTCTGGCTGCTGGCAGCAAGGCTGTGGGGCCTGGGCATTGGG
AlaValTrpLeuLeuAlaAlaArgLeuTrpGlyLeuGlyIleGly

226 GCTGAGGTGTGGTGGAACCTTGTGCCGCGTAAGACAGTGTCTTCT
AlaGluValTrpTrpAsnLeuValProArgLysThrValSerSer

271 GGGGAGCTGGCCACGGTAGTACGGCGGTTCTCCCAGACCGGCATC
GlyGluLeuAlaThrValValArgArgPheSerGlnThrGlyIle

316 CAGGACTTCCTGACACTGACGCTGACGGAGCCCACTGGGCTTCTG
GlnAspPheLeuThrLeuThrLeuThrGluProThrGlyLeuLeu

361 TACGTGGGCGCCCGAGAGGCCCTGTTTGCCTTCAGCATGGAGGCC
TyrValGlyAlaArgGluAlaLeuPheAlaPheSerMetGluAla

406 CTGGAGCTGCAAGGAGCGATCTCCTGGGAGGCCCCCGTGGAGAAG
LeuGluLeuGlnGlyAlaIleSerTrpGluAlaProValGluLys

451 AAGACTGAGTGTATCCAGAAAGGGAAGAACAACCAGACCGAGTGC
LysThrGluCysIleGlnLysGlyLysAsnAsnGlnThrGluCys

496 TTCAACTTCATCCGCTTCCTGCAGCCCTACAATGCCTCCCACCTG
PheAsnPheIleArgPheLeuGlnProTyrAsnAlaSerHisLeu

541 TACGTCTGTGGCACCTACGCCTTCCAGCCCAAGTGCACCTACGTC
TyrValCysGlyThrTyrAlaPheGlnProLysCysThrTyrVal

586 AACATGCTCACCTTCACTTTGGAGCATGGAGAGTTTGAAGATGGG
AsnMetLeuThrPheThrLeuGluHisGlyGluPheGluAspGly

631 AAGGGCAAGTGTCCCTATGACCCAGCTAAGGGCCATGCTGGCCTT
LysGlyLysCysProTyrAspProAlaLysGlyHisAlaGlyLeu

676 CTTGTGGATGGTGAGCTGTACTCGGCCACACTCAACAACTTCCTG
LeuValAspGlyGluLeuTyrSerAlaThrLeuAsnAsnPheLeu

721 GGCACGGAACCCATTATCCTGCGTAACATGGGGCCCCACCACTCC
GlyThrGluProIleIleLeuArgAsnMetGlyProHisHisSer

766 ATGAAGACAGAGTACCTGGCCTTTTGGCTCAACGAACCTCACTTT
MetLysThrGluTyrLeuAlaPheTrpLeuAsnGluProHisPhe

811 GTAGGCTCTGCCTATGTACCTGAGAGTGTGGGCAGCTTCACGGGG
ValGlySerAlaTyrValProGluSerValGlySerPheThrGly

856 GACGACGACAAGGTCTACTTCTTCTTCAGGGAGCGGGCAGTGGAG
AspAspAspLysValTyrPhePhePheArgGluArgAlaValGlu

Fig. 11

901 TCCGACTGCTATGCCGAGCAGGTGGTGGCTCGTGTGGCCCGTGTC
SerAspCysTyrAlaGluGlnValValAlaArgValAlaArgVal

946 TGCAAGGGCGATATGGGGGGCGCACGGACCCTGCAGAGGAAGTGG
CysLysGlyAspMetGlyGlyAlaArgThrLeuGlnArgLysTrp

991 ACCACGTTCCTGAAGGCGCGGCTGGCATGCTCTGCCCCGAACTGG
ThrThrPheLeuLysAlaArgLeuAlaCysSerAlaProAsnTrp

1036 CAGCTCTACTTCAACCAGCTGCAGGCGATGCACACCCTGCAGGAC
GlnLeuTyrPheAsnGlnLeuGlnAlaMetHisThrLeuGlnAsp

1081 ACCTCCTGGCACAACACCACCTTCTTTGGGGTTTTTCAAGCACAG
ThrSerTrpHisAsnThrThrPhePheGlyValPheGlnAlaGln

1126 TGGGGTGACATGTACCTGTCGGCCATCTGTGAGTACCAGTTGGAA
TrpGlyAspMetTyrLeuSerAlaIleCysGluTyrGlnLeuGlu

1171 GAGATCCAGCGGGTGTTTGAGGGCCCCTATAAGGAGTACCATGAG
GluIleGlnArgValPheGluGlyProTyrLysGluTyrHisGlu

1216 GAAGCCCAGAAGTGGGACCGCTACACTGACCCTGTACCCAGCCCT
GluAlaGlnLysTrpAspArgTyrThrAspProValProSerPro

1261 CGGCCTGGCTCGTGCATTAACAACTGGCATCGGCGCCACGGCTAC
ArgProGlySerCysIleAsnAsnTrpHisArgArgHisGlyTyr

1306 ACCAGCTCCCTGGAGCTACCCGACAACATCCTCAACTTCGTCAAG
ThrSerSerLeuGluLeuProAspAsnIleLeuAsnPheValLys

1351 AAGCACCCGCTGATGGAGGAGCAGGTGGGGCCTCGGTGGAGCCGC
LysHisProLeuMetGluGluGlnValGlyProArgTrpSerArg

1396 CCCCTGCTCGTGAAGAAGGGCACCAACTTCACCCACCTGGTGGCC
ProLeuLeuValLysLysGlyThrAsnPheThrHisLeuValAla

1441 GACCGGGTTACAGGACTTGATGGAGCCACCTATACAGTGCTGTTC
AspArgValThrGlyLeuAspGlyAlaThrTyrThrValLeuPhe

1486 ATTGGCACAGGAGACGGCTGGCTGCTCAAGGCTGTGAGCCTGGGG
IleGlyThrGlyAspGlyTrpLeuLeuLysAlaValSerLeuGly

1531 CCCTGGGTTCACCTGATTGAGGAGCTGCAGCTGTTTGACCAGGAG
ProTrpValHisLeuIleGluGluLeuGlnLeuPheAspGlnGlu

1576 CCCATGAGAAGCCTGGTGCTATCTCAGAGCAAAAAGCTGCTCTTT
ProMetArgSerLeuValLeuSerGlnSerLysLysLeuLeuPhe

1621 GCCGGCTCCCGCTCTCAGCTGGTGCAGCTGCCCGTGGCCGACTGC
AlaGlySerArgSerGlnLeuValGlnLeuProValAlaAspCys

1666 ATTAAGTATCGCTCCTGTGCAGACTGTGTCCTCGCCCGGGACCCC
IleLysTyrArgSerCysAlaAspCysValLeuAlaArgAspPro

Fig. 11 Continued

1711 TATTGCGCCTGGAGCGTCAACACCAGCCGCTGTGTGGCCGTGGGT
TyrCysAlaTrpSerValAsnThrSerArgCysValAlaValGly

1756 GGCCACTCTGGATCTCTACTGATCCAGCATGTGATGACCTCGGAC
GlyHisSerGlySerLeuLeuIleGlnHisValMetThrSerAsp

1801 ACTTCAGGCATCTGCAACCTCCGTGGCAGTAAGAAAGTCAGGCCC
ThrSerGlyIleCysAsnLeuArgGlySerLysLysValArgPro

1846 ACTCCCAAAAACATCACGGTGGTGGCGGGCACAGACCTGGTGCTG
ThrProLysAsnIleThrValValAlaGlyThrAspLeuValLeu

1891 CCCTGCCACCTCTCCTCCACTTGGCCCCGGGGTTCAGTGGTATTT
ProCysHisLeuSerSerThrTrpProArgGlySerValValPhe

1936 TATACTTGCCTTCTTCCTGTACAGGGCTGGGAAAGGCTGTGTGAG
TyrThrCysLeuLeuProValGlnGlyTrpGluArgLeuCysGlu

1981 GGGAAAAAAAGGAAAGGGTGGGCCTGCTGTGGACAATGGCATACT
GlyLysLysArgLysGlyTrpAlaCysCysGlyGlnTrpHisThr

2026 CTCTTCCAGCCCTAGGAGGAGGGCTCCTAACAGTGTAACTTATTG
LeuPheGlnPro

2071 TGTCCCCGCGTATTTATTTGTTGTAAATATTTGAGTATTTTTATA
2116 TTGACAAATAAAATGGAGAAAATGAAAAAAAAAAAAAAAAA

Fig. 11 Continued

```
  1 CGCTCCATGTATNAGTTTCATGCAGGCTCTTGGGAAAGCTGGTGC
           MetTyr---PheHisAlaGlySerTrpGluSerTrpCys

 46 TGCTGCTGCCTGATTCCCGCCGACAGACCTTGGGACCGGGGCCAA
    CysCysCysLeuIleProAlaAspArgProTrpAspArgGlyGln

 91 CACTGGCAGCTGGAGATGGCGGACACGAGATCCGTGCACGAGACT
    HisTrpGlnLeuGluMetAlaAspThrArgSerValHisGluThr

136 AGGTTTGAGGCGGCCGTGAAGGTGATCCAGAGTTTGCCGAAGAAT
    ArgPheGluAlaAlaValLysValIleGlnSerLeuProLysAsn

181 GATTCATTCCAGCCAACAAATGAAATGATGCTTAAATTTTATAGC
    AspSerPheGlnProThrAsnGluMetMetLeuLysPheTyrSer

226 TTCTATAAGCAGGCAACTGAAGGACCCTGTAAACTTTCAAGGCCT
    PheTyrLysGlnAlaThrGluGlyProCysLysLeuSerArgPro

271 GGATTTTGGGATCCTATTGGAAGATATAAATGGGATGCTTGGAGT
    GlyPheTrpAspProIleGlyArgTyrLysTrpAspAlaTrpSer

316 TCACTGGGTGATATGACCAAAGAGGAAGCCATGATTGCATATGTT
    SerLeuGlyAspMetThrLysGluGluAlaMetIleAlaTyrVal

361 GAAGAAATGAAAAAGATTATTGAAACTATGCCAATGACTGAGAAA
    GluGluMetLysLysIleIleGluThrMetProMetThrGluLys

406 GTTGAAGAATTGCTGCGTGTCATAGGTCCATTTTATGAAATTGTC
    ValGluGluLeuLeuArgValIleGlyProPheTyrGluIleVal

451 GAGGACAAAAAGAGTGGCAGGAGTTCTGATATAACCTCAGTCCGA
    GluAspLysLysSerGlyArgSerSerAspIleThrSerValArg

496 CTGGAGAAAATCTCTAAATGTTTAGAAGATCTTGGTAATGTTCTC
    LeuGluLysIleSerLysCysLeuGluAspLeuGlyAsnValLeu

541 ACTTCTACTCCAAACGCCAAAACCGTTAATGGTAAAGCTGAAAGC
    ThrSerThrProAsnAlaLysThrValAsnGlyLysAlaGluSer

586 AGTGACAGTGGAGCCGAGTCTGAGGAAGAAGAGGCCCAAGAAGAA
    SerAspSerGlyAlaGluSerGluGluGluGluAlaGlnGluGlu

631 GTGAAAGGAGCAGAACAAAGTGATAATGATAAGAAAATGATGAAG
    ValLysGlyAlaGluGlnSerAspAsnAspLysLysMetMetLys

676 AAGTCAGCAGACCATAAGAATTTGGAAGTCATTGTCACTAATGGC
    LysSerAlaAspHisLysAsnLeuGluValIleValThrAsnGly

721 TATGATAAAGATGGCTTTGTTCAGGATATACAGAATGACATTCAT
    TyrAspLysAspGlyPheValGlnAspIleGlnAsnAspIleHis

766 GCCAGTTCTTCCCTGAATGGCAGAAGCACTGAAGAAGTAAAGCCC
    AlaS rSerSerLeuAsnGlyArgSerThrGluGluValLysPro
```

Fig. 12

811 ATTGATGAAAACTTGGGGCAAACTGGAAAATCTGCTGTTTGCATT
IleAspGluAsnLeuGlyGlnThrGlyLysSerAlaValCysIle

856 CACCAAGATATAAATGATGATCATGTTGAAGATGTTACAGGAATT
HisGlnAspIleAsnAspAspHisValGluAspValThrGlyIle

901 CAGCATTTGACAAGCGATTCAGACAGTGAAGTTTACTGTGATTCT
GlnHisLeuThrSerAspSerAspSerGluValTyrCysAspSer

946 ATGGAACAATTTGGACAAGAAGAGTCTTTAGACAGCTTTACGTCC
MetGluGlnPheGlyGlnGluGluSerLeuAspSerPheThrSer

991 AACAATGGACCATTTCAGTATTACTTGGGTGGTCATTCCAGTCAA
AsnAsnGlyProPheGlnTyrTyrLeuGlyGlyHisSerSerGln

1036 CCCATGGAAAATTCTGGATTTCGTGAAGATATTCAAGTACCTCCT
ProMetGluAsnSerGlyPheArgGluAspIleGlnValProPro

1081 GGAAATGGCAACATTGGGAATATGCAGGTGGTTGCAGTTGAAGGA
GlyAsnGlyAsnIleGlyAsnMetGlnValValAlaValGluGly

1126 AAAGGTGAAGTCAAGCATGGAGGAGAAGATGGCAGGAATAACAGC
LysGlyGluValLysHisGlyGlyGluAspGlyArgAsnAsnSer

1171 GGAGCACCACACCGGGAGAAGCGAGGCGGAGAAACTGACGAATTC
GlyAlaProHisArgGluLysArgGlyGlyGluThrAspGluPhe

1216 TCTAATGTTAGAAGAGGAAGAGGACATAGGATGCAACACTTGAGC
SerAsnValArgArgGlyArgGlyHisArgMetGlnHisLeuSer

1261 GAAGGAACCAAGGGCCGGCAGGTGGGAAGTGGAGGTGATGGGGAG
GluGlyThrLysGlyArgGlnValGlySerGlyGlyAspGlyGlu

1306 CGCTGGGGCTCCGACAGAGGGTCCCGAGGCAGCCTCAATGAGCAG
ArgTrpGlySerAspArgGlySerArgGlySerLeuAsnGluGln

1351 ATCGCCCTCGTGCTGATGAGACTGCAGGAGGACATGCAGAATGTC
IleAlaLeuValLeuMetArgLeuGlnGluAspMetGlnAsnVal

1396 CTTCAGAGACTGCAGAAACTGGAAACGCTGACTGCTTTGCAGGCA
LeuGlnArgLeuGlnLysLeuGluThrLeuThrAlaLeuGlnAla

1441 AAATCATCAACATCAACATTGCAGACTGCTCCTCAGCCCACCTCA
LysSerSerThrSerThrLeuGlnThrAlaProGlnProThrSer

1486 CAGAGACCATCTTGGTGGCCCTTCGAGATGTCTCCTGGTGTGCTA
GlnArgProSerTrpTrpProPheGluMetSerProGlyValLeu

1531 ACGTTTGCCATCATATGGCCTTTTATTGCACAGTGGTTGGTGTAT
ThrPheAlaIleIleTrpProPheIleAlaGlnTrpLeuValTyr

Fig. 12 Continued

1576 TTATACTATCAAAGAAGGAGAAGAAAACTGAACTGAGGAAAATGG
LeuTyrTyrGlnArgArgArgArgLysLeuAsn

1621 TGTTTTCCTCAAGAAGACTACTGGAACTGGATGACCTCAGAATGA
1666 ACTGGATTGTGGTGTTCACAAGAAAATCTTAGTTTGTGATGATTA
1711 CATTGCTTTTTGTTGTCCAGTAGTTTAGTTTGTGTACATATATAC
1756 ACATATATATTTTGCACTACACAAACGATAACATTTTAAGGACTA
1801 ATATTGCTGATACTTGAATAATCAATCTCTACTAGGTTATAAGTA
1846 GTATACACAGATTTACCCTGCCCTTGAACTTGAAGGACATTAAAT
1891 TATTAATGATCATTTGGTAACATGTTTACCTGATTATCTTCCATA
1936 GAGTAACATAAGCTGCTTTTCAAAGGTACCATTGTGATAATGAGA
1981 TCAAATTTATAAGTTATTATTTTTAATTTTCTAAATTAAATAAAA
2026 GAAAGAATGCAAAAAAAAAAAAAAAAAAAAA

Fig. 12 Continued

```
                               .         .         .         .         .
20936375-0-104:    1 ..MYXFHAGSWESWCCCCLIPADRPWDRGQHWQLEMADTRSVHETRFEAA 48
                       ||||||||||||||||||||||||||||||||||||||||||||||
20936375.0.1:      1 MLFLSFHAGSWESWCCCCLIPADRPWDRGQHWQLEMADTRSVHETRFEAA 50

                 .         .         .         .         .
  49 VKVIQSLPKNDSFQPTNEMMLKFYSFYKQATEGPCKLSRPGFWDPIGRYK 98
     |||||||||| |||||||||||||||||||||||||||||||||||||||
  51 VKVIQSLPKNGSFQPTNEMMLKFYSFYKQATEGPCKLSRPGFWDPIGRYK 100

                 .         .         .         .         .
  99 WDAWSSLGDMTKEEAMIAYVEEMKKIIETMPMTEKVEELLRVIGPFYEIV 148
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 101 WDAWSSLGDMTKEEAMIAYVEEMKKIIETMPMTEKVEELLRVIGPFYEIV 150

                 .         .         .         .         .
 149 EDKKSGRSSDITSVRLEKISKCLEDLGNVLTSTPNAKTVNGKAESSDSGA 198
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 151 EDKKSGRSSDITSVRLEKISKCLEDLGNVLTSTPNAKTVNGKAESSDSGA 200

                 .         .         .         .         .
 199 ESEEEEAQEEVKGAEQSDNDKKMMKKSADHKNLEVIVTNGYDKDGFVQDI 248
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 201 ESEEEEAQEEVKGAEQSDNDKKMMKKSADHKNLEVIVTNGYDKDGFVQDI 250

                 .         .         .         .         .
 249 QNDIHASSSLNGRSTEEVKPIDENLGQTGKSAVCIHQDINDDHVEDVTGI 298
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 251 QNDIHASSSLNGRSTEEVKPIDENLGQTGKSAVCIHQDINDDHVEDVTGI 300

                 .         .         .         .         .
 299 QHLTSDSDSEVYCDSMEQFGQEESLDSFTSNNGPFQYYLGGHSSQPMENS 348
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 301 QHLTSDSDSEVYCDSMEQFGQEESLDSFTSNNGPFQYYLGGHSSQPMENS 350

                 .         .         .         .         .
 349 GFREDIQVPPGNGNIGNMQVVAVEGKGEVKHGGEDGRNNSGAPHREKRGG 398
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 351 GFREDIQVPPGNGNIGNMQVVAVEGKGEVKHGGEDGRNNSGAPHREKRGG 400

                 .         .         .         .         .
 399 ETDEFSNVRRGRGHRMQHLSEGTKGRQVGSGGDGERWGSDRGSRGSLNEQ 448
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 401 ETDEFSNVRRGRGHRMQHLSEGTKGRQVGSGGDGERWGSDRGSRGSLNEQ 450

                 .         .         .         .         .
 449 IALVLMRLQEDMQNVLQRLQKLETLTALQAKSSTSTLQTAPQPTSQRPSW 498
     ||||||||||||||||||||||||| ||||||||||||||||||||||||
 451 IALVLMRLQEDMQNVLQRLQKLEMLTALQAKSSTSTLQTAPQPTSQRPSW 500

                 .         .         .
 499 WPFEMSPGVLTFAIIWPFIAQWLVYLYYQRRRRKLN 534
     ||||||||||||||||||||||||||||||||||||
 501 WPFEMSPGVLTFAIIWPFIAQWLVYLYYQRRRRKLN 536
```

Fig. 13

Sequences analyzed:

1. 1795045-0-77
2. 1795045-0-61

```
1795045077          MKNQVCSKCGEGTYSLGSGIKFDEWDELPAGFSNIATFMDTVVGPSDSRPDGCNNSSWIP
1795045061          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~MHSSWIP

1795045077          RGNYIESNRDDCTVSLIYAVHLKKSGYVFFEYQYVDNNIFFEFFIQNDQCQEMDTTTDKW
1795045061          RGNYIESNRDDCTVSLIYAVHLKKSGYVFFEYQYVDNNIFFEFFIQNDQCQEMDTTTDKW

1795045077          VKLTDNGEWGSHSVMLKSGTNILYWRTTGILMGSKAVKPVLVKNITIEGVAYTSECFPCK
1795045061          VKLTDNGEWGSHSVMLKSGTNILYWRTTGILMGSKAVKPVLVKNITIEGVAYTSECFPCK

1795045077          PGTFSNKPGSFNCQVCPRNTYSEKGAKECIRCKDDSQFSEEGSSECTERPPCTTKDYFQI
1795045061          PGTFSNKPGSFNCQVCPRNTYSEKGAKECIRCKDDSQFSEEGSSECTERPPCTTKDYFQI

1795045077          HTPCDEEGKTQIMYKWIEPKICREDLTDAIRLPPSGEKKDCPPCNPGFYNNGSSSCHPCP
1795045061          HTPCDEEGKTQIMYKWIEPKICREDLTDAIRLPPSGEKKDCPPCNPGFYNNGSSSCHPCP

1795045077_cura_56  PGTFSDGTKECRPCPAGTEPALGFEYKWWNVLPGNMKTSCFNVGNSKCDGMNGWEVAGDH
1795045061_cura_54  PGTFSDGTKECRPCPAGTEPALGFEYKWWNVLPGNMKTSCFNVGNSKCDGMNGWEVAGDH

1795045077_cura_56  IQSGAGGSDNDYLIILNLHIPGFKPPTSMTGATGSELGRITFVFETLCSADCVLYFMVDIN
1795045061_cura_54  IQSGAGGSDNDYLIILNLHIPGFKPPTSMTGATGSELGRITFVFETLCSADCVLYFMVDIN

1795045077_cura_56  RKSTNVVESWGGTKEKQAYTHIIFKNATFTFTWGIPRELIQGPR
1795045061_cura_54  RKSTNVVESWGGTKEKQAYTHIIFKNATFTFTWGIPRELIQGPR
```

Fig. 14

Sequences analyzed:

1. **20422974-0-132-ext-2_Cura_56**
2. **Q64151_SEMAPHORIN_4C_PREC_Mus**
3. **Q92854_SEMAPHORIN**
4. **20422974.2_Cura_54**
5. **20422974.0.132_Cura_54**

```
204229740132ext2_cura_56        MAPHWAVWLLAARLWGLGIGAEVWWNLVPRKTVSSGELATVVRRFSQTGIQDFLTLTLTE
204229740132_cura_54            MAPHWAVWLLAARLWGLGIGAEVWWNLVPRKTVSSGELATVVRRFSQTGIQDFLTLTLTE
204229742_cura_54               MAPHWAVWLLAARLWGLGIGAEVWWNLVPRKTVSSGELATVVRRFSQTGIQDFLTLTLTE
q64151_semaphorin_4c_prec_mus   MAPHWAVWLLAAGLWGLGIGAEMWWNLVPRKTVSSGELAVVVRRFSQTGIQDFLTLTLTE
q92854_semaphorin               MRMCTPIRGLLMAL.AVMFGTAMAFAPIPRITWEHREVHLV..QFHEPDIYNYSALLLSE

204229740132ext2_cura_56        PTGLLYVGAREALFAF.SMEALELQGAISWEAPVEKKTECIQKGKNNQTECFNFIRFLQP
204229740132_cura_54            PTGLLYVGAREALFAF.SMEALELQGAISWEAPVEKKTECIQKGKNNQTECFNFIRFLQP
204229742_cura_54               PTGLLYVGAREALFAF.SMEALELQGAISWEAPVEKKTECIQKGKNNQTECFNFIRFLQP
q64151_semaphorin_4c_prec_mus   HSGLLYVGAREALFAF.SVEALELQGAISWEAPAEKKIECTQKGKSNQTECFNFIRFLQP
q92854_semaphorin               DKDTLYIGAREAVFAVNALNISEKQHEVYWKVSEDKKAKCAEKGKSKQTECLNYIRVLQP

204229740132ext2_cura_56        YNASHLYVCGTYAFQPKCTYVNMLTFTLEHGEFEDGKGKCPYDPAKGHAGLLVDGELYSA
204229740132_cura_54            YNASHLYVCGTYAFQPKCTYVNMLTFTLEHGEFEDGKGKCPYDPAKGHAGLLVDGELYSA
204229742_cura_54               YNASHLYVCGTYAFQPKCTYVNMLTFTLEHGEFEDGKGKCPYDPAKGHAGLLVDGELYSA
q64151_semaphorin_4c_prec_mus   YNSSHLYVCGTYAFQPKCTYINMLTFTLDRAEFEDGKGKCPYDPAKGHTGLLVDGELYSA
q92854_semaphorin               LSATSLYVCGTNAFQPACDHLNLTSFKF.LGKNEDGKGRCPFDPAHSYTSVMVDGELYSG

204229740132ext2_cura_56        TLNNFLGTEPIILRNMGPHHSMKTEYLAFWLNEPHFVGSAYVPESVGSFTGDDDKVYFFF
204229740132_cura_54            TLNNFLGTEPIILRNMGPHHSMKTEYLAFWLNEPHFVGSAYVPESVGSFTGDDDKVYFFF
204229742_cura_54               TLNNFLGTEPIILRNMGPHHSMKTEYLAFWLNEPHFVGSAYVPESVGSFTGDDDKVYFFF
q64151_semaphorin_4c_prec_mus   TLNNFLGTEPVILRYMGTHHSIKTEYLAFWLNEPHFVGSAFVPESVGSFTGDDDKIYFFF
q92854_semaphorin               TSYNFLGSEPIISRN.SSHSPLRTEYAIPWLNEPSFVFADVIRKSPDSPDGEDDRVYFFF

204229740132ext2_cura_56        RERAVESDCYAEQVVARVARVCKGDMGGARTLQRKWTTFLKARLACSAPNWQLYFNQLQA
204229740132_cura_54            RERAVESDCYAEQVVARVARVCKGDMGGARTLQRKWTTFLKARLACSAPNWQLYFNQLQA
204229742_cura_54               RERAVESDCYAEQVVARVARVCKGDMGGARTLQRKWTTFLKARLACSAPNWQLYFNQLQA
q64151_semaphorin_4c_prec_mus   SERAVEYDCYSEQVVARVARVCKGDMGGARTLQKKWTTFLKARLVCSAPDWKVYFNQLKA
q92854_semaphorin               TEVSVEYEFVFRVLIPRIARVCKGDQGGLRTLQKKWTSFLKARLICSRPDSGLVFNVLRD
```

Fig. 15A

```
204229740132ext2_cura_56       MHTLQDTSWHNTTFFGVFQAQWGDMYLSAICEYQLEEIQRVF.EGPYKE...YHEEAQKW
204229740132_cura_54           MHTLQDTSWHNTTFFGVFQAQWGDMYLSAICEYQLEEIQRVF.EGPYKE...YHEEAQKW
204229742_cura_54              MHTLQDTSWHNTTFFGVFQAQWGDMYLSAICEYQLEEIQRVF.EGPYKE...YHEEAQKW
q64151_semaphorin_4c_prec_mus  VHTLRGASWHNTTFFGVFQARWGCMDLSAVCEYQLEQIQQVF.EGPYKE...YSEQAQKW
q92854_semaphorin              VFVLRSPGLKVPVFYALFTFQLNNVGLSAVCAYNLSTAEEVFSHGKYMQSTTVEQSHTKW

204229740132ext2_cura_56       DRYTDPVPSPRPGSCINNWHRRHGYTSSLELPDNILNFVKKHPLMEEQVGPRWSRPLLVK
204229740132_cura_54           DRYTDPVPSPRPGSCINNWHRRHGYTSSLELPDNILNFVKKHPLMEEQVGPRWSRPLLVK
204229742_cura_54              DRYTDPVPSPRPGSCINNWHRRHGYTSSLELPDNILNFVKKHPLMEEQVGPRWSRPLLVK
q64151_semaphorin_4c_prec_mus  ARYTDPVPSPRPGSCINNWHRDNGYTSSLELPDNTLNFIKKHPLMEDQVKPRLGRPLLVK
q92854_semaphorin              VRYNGPVPKPRPGACIDSEARAANYTSSLNLPDKTLQFVKDHPLMDDSVTPIDNRPRLLK

204229740132ext2_cura_56       KGTNFTHLVADRVTGLDGATYTVLFIGTGDGWLLKAVSLGPWVHLIEELQLF.DQEPMRS
204229740132_cura_54           KGTNFTHLVADRVTGLDGATYTVLFIGTGDGWLLKAVSLGPWVHLIEELQLF.DQEPMRS
204229742_cura_54              KGTNFTHLVADRVTGLDGATYTVLFIGTGDGWLLKAVSLGPWVHLIEELQLF.DQEPMRS
q64151_semaphorin_4c_prec_mus  KNTNFTHVVADRVPGLDGATYTVLFIGTGDGWLLKAVSLGPWIHMVEELQVF.DQEPVES
q92854_semaphorin              KDVNYTQIVVDRTQALDGTVYDVMFVSTDRGALHKAISLEHAVHIIEETQLFQDFEPVQT

204229740132ext2_cura_56       LVLSQSK..KLLFAGSRSQLVQLPVADCIKYRSCADCVLARDPYCAWSVNTSRCVA.VGG
204229740132_cura_54           LVLSQSK..KLLFAGSRSQLVQLPVADCIKYRSCADCVLARDPYCAWSVNTSRCVA.VGG
204229742_cura_54              LVLSQSK..KLLFAGSRSQLVQLPVADCIKYRSCADCVLARDPYCAWSVNTSRCVA.VGG
q64151_semaphorin_4c_prec_mus  LVLSQSK..KVLFAGSRSQLVQLSIADCTKYRFCVDCVLARDPYCAWNVNTSRVVATTSG
q92854_semaphorin              LILSSKKGNRFVYAGSNSGVVQAPLAFCGKHGTCEDCVLARDPYCAWSPPTATCVALHQT

204229740132ext2_cura_56       HSGSLLIQHVMTSDTSGICNLRGSK.KVRPTPKNITVVAGTDLVLPCHLSSTWPRCSVVF
204229740132_cura_54           HFGSLLIQHVMTSDTSGICNLRGSK.KVRPTPKNITVVAGTDLVLPCHLSSTWPRCSVVF
204229742_cura_54              HFGSLLIQHVMTSDTSGICNLRGSKIQSGPLPKNITVVAGTDLVLPCHLSSNLALPDSNP
q64151_semaphorin_4c_prec_mus  RSGSFLVQHVANLDTSKMCNQYGIK.KVRSIPKNITVVSGTDLVLPCHLSSNLAHAHWTF
q92854_semaphorin              ESPSRGLIQEMSGDAS.VC.....PDKSKGSYRQHFFKHGGTAELKCSQKSNLARVFWKE

204229740132ext2_cura_56       YTCLLPVQGWERLCEGKKRKGWACCGQWHTLFQP~~~~~~~~~~~~~~~~~~~~~~~~~~
204229740132_cura_54           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
204229742_cura_54              EESSV~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
q64151_semaphorin_4c_prec_mus  GSQDLPAEQPGSFLYDTGLQALVVMAAQSRHSGPYRCYSEEQGTRLAAESYLVAVVAGSS
q92854_semaphorin              QNGVLKAESPKYGLMGRKNLLIFNLSEGDSGVYQCLSEERVKNKTVFQVVAKHVLEVKVV

204229740132ext2_cura_56       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
204229740132_cura_54           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
204229742_cura_54              ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
q64151_semaphorin_4c_prec_mus  VTLEARAPLENLGLVWLAVVALGAVCLVLLLLVLSLRRRLREELEKGAKASERTLVYPLE
q92854_semaphorin              PKPVVAPTLSVVQTEGSRIATKVLVASTQGSSPPTPAVQATSSGAITLPPKPAPTGTSCE
```

Fig. 15B

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204229740132ext2_cura_56       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
204229740132_cura_54           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
204229742_cura_54              ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
q64151_semaphorin_4c_prec_mus  LPKEPASPPFRPGPETDEKLWDPVGYYYSDGSLKIVPGHARCQPGGGPPSPPPGIPGQPL
q92854_semaphorin              PKIVINTVPQLHSEKTMYLKSSDNRLLMSLFLFFFVLFLCLFFYNCYKGYLPRQCLKFRS

204229740132ext2_cura_56       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
204229740132_cura_54           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
204229742_cura_54              ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
q64151_semaphorin_4c_prec_mus  PSPTRLHLGGGRNSNANGYVRLQLGGEDRGGSGHPLPELADELRRKLQQRQPLPDSNPEE
q92854_semaphorin              ALLIGKKKPKSDFCDREQSLKETLVEPGSFSQQNGEHPKPALDTGYETEQDTITSKVPTD

204229740132ext2_cura_56       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
204229740132_cura_54           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
204229742_cura_54              ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
q64151_semaphorin_4c_prec_mus  SSV~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
q92854_semaphorin              REDSQRIDDLSARDKPFDVKCELKFADSDADGD
```

Fig. 15C

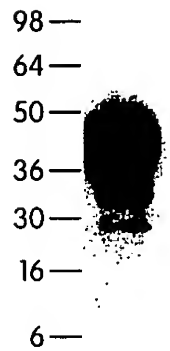

Fig. 16

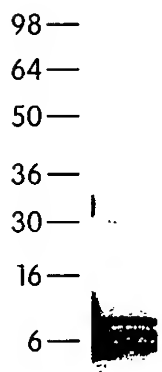

Fig. 17

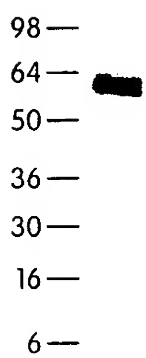

Fig. 18

	Relative Expression (%)				
Tissue Source	3445452	17089878	1795045.0.61	20422974	20936375.0.104
Endothelial cells	0.00	0.00	1.88	1.11	8.72
Endothelial cells (treated)	0.00	0.01	4.58	1.99	9.74
Pancreas	2.05	0.32	2.68	5.63	16.49
Pancreatic ca. CAPAN 2	0.01	0.00	0.07	1.91	40.05
Adipose	0.24	1.48	6.70	10.01	51.05
Adrenal gland	0.92	0.43	1.36	9.54	75.26
Thyroid	21.17	0.00	1.96	6.25	30.78
Salivary glands	7.59	0.13	1.56	5.67	24.66
Pituitary gland	0.05	0.07	1.11	10.73	10.81
Brain (fetal)	0.17	15.18	3.59	12.41	25.00
Brain (whole)	1.96	34.15	52.85	28.32	38.16
Brain (amygdala)	1.03	19.89	7.13	7.97	46.33
Brain (cerebellum)	4.64	29.73	76.84	29.32	55.86
Brain (hippocampus)	2.98	28.32	27.17	33.45	57.04
Brain (hypothalamus)	10.51	1.18	12.67	4.12	38.69
Brain (substantia nigra)	6.25	7.18	23.49	16.61	67.36
Brain (thalamus)	4.80	6.00	22.53	13.68	69.26
Spinal cord	1.76	4.24	7.64	29.12	50.70
CNS ca. (glio/astro) U87-MG	0.03	0.00	1.99	2.16	29.73
CNS ca. (glio/astro) U-118-MG	0.00	3.54	1.25	2.34	12.33
CNS ca. (astro) SW1783	0.00	0.17	0.00	0.74	13.03
CNS ca.* (neuro;met) SK-N-AS	0.00	0.43	4.30	10.01	93.95
CNS ca. (astro) SF-539	0.07	0.14	0.00	9.81	14.16
CNS ca. (astro) SNB-75	0.00	0.06	0.23	11.58	8.84
CNS ca. (glio) SNB-19	0.01	0.58	0.11	5.15	33.45
CNS ca. (glio) U251	0.01	0.00	0.01	1.58	8.42
CNS ca. (glio) SF-295	0.00	0.00	0.01	3.77	10.44
Heart	33.92	0.01	1.82	7.64	100.00
Skeletal muscle	100.00	0.00	1.00	3.06	79.00
Bone marrow	1.05	3.72	0.43	1.69	18.17
Thymus	0.30	0.21	4.42	6.12	28.52
Spleen	0.14	0.13	2.59	17.43	24.49
Lymph node	0.28	0.28	1.92	10.51	11.74

Fig. 19

SECX	Clone Number	Tissue Expression	Length (nt)	ORF (nt)	Amine Acid Length	Calculate Molecular Weight of Encoded Protein	Protein Similarity (BLASTP Non-Redundant Composite Database)	Protein Similarity (Human Sequence)	Signal Peptide Cleavage Site (nt)	Cellular Localization
1	3445452	Prostate Gland	932	113-796	227	25734.1	Identities 52/128 (40%); Positives 72/128 (56%) with ACC:P31044 Phosphatidylethanolamine-Binding Protein (PEBP); 23Kd Morphine_Binding Protein (P23K) *Rattus norvegicus*. 187 amino acid residues.	Identities 44/120 (36%); Positives 66/120 (55%) with ACC:P31044 Phosphatidylethanolamine-Binding Protein (PEBP) *Homo sapiens*. 186 Amino Acid residues.	yyyy. Most likely cleavage site between positions 22 and 23: VTG-DE.	Outside - Cert=0.7380. Apears to possess a cleavable N-terminal Signal Sequence.
2	4011999	Not Known	734	66-(?)735	223	24499	Identities 55/76 (72%) Positives 61/76 (80%) with ptnr:SPTREMBL-ACC:Q13670 PMS2-Related Protein HPMSR6 *Homo sapiens*. 270 amino acid residues.	Identities 48/127 (37%); Positives 69/127 (54%) with ptnr: SPTREMBL-ACC:075631 Uroplakin III *Homo sapiens*. 287 amino acid residues.	yyyy. Most likely cleavage site between positions 27 and 28: SLS-LD.	Plasma Membrane - Cert.=0.8056. Appears to possess a cleavable N-terminal Signal Sequence.
3	17089878.0.5	Fetal Brain	2762	264-2630	788	88337	Identities 729/788 (92%); Positives 758/788 (96%) with ACC:P79995 Cadherin-10 Precursor *Gallus gallus*. 789 amino acid residues. Identities 636/650 (97%); Positives 645/650 (99%) with rat cadherin-10. 653 amino acid residues.	Identities 577/790 (73%); Positives 676/790 (85%) with ACC:P55285 Cadherin-6 Precursor (Kidney-Cahedrin) *Homo sapiens*. 790 amino acid residues.	yyyy. Most likely cleavage site between positions 22 and 23:CSECX-EI.	Plasma Membrane - Cert.=0.4600. Appears to possess a cleavable N-terminal Signal Sequence.
4	17089878.0.6	Fetal Brain	1820	285-1704	473	529226	Identities 445/473 (94%); Positives 465/473 (98%) with ACC:P7995 789 aa Cadherin-10 Precursor	Identities 346/476 (72%); Positives 415/476 (87%) with ACC:P55285, human Cadherin-6 precursor Precursor (790 aa)		Plasma Membrane - Cert.=0.7000. Apparently lacks cleavable N-terminal Signal Sequences.

Fig. 20A

SEC No.	Clone Number	Tissue Expression	Nucleo tide Length	Open Reading Frame (nt)	Amine Acid Length	Calculate Molecular Weight	Protein Similarity (BLASTP Non-Redundant Composite Database)	Protein Similarity (Human Sequence)	Signal Peptide Cleavage Site (nt)	Cellular Localization
5	1795045.0.61	Brain, Thalamus, Pituitary Gland	1508	226-1461	411	46054.5	Identities 51/198 (25%); Positives 71/198 (35%) with ACC:O00276 Lymphocyte-Associated Receptor of Death 2 *Homo sapiens*. 510 amino acid residues.	Identities 51/198 (25%); Positives 71/198 (35%) with ACC:O00276 Lymphocyte-Associated Receptor of Death 2 *Homo sapiens*. 510 amino acid residues.		Cytoplam- Cert.=0.4500. Appears to possess no cleavable N-terminal Signal Sequence.
6	20422974.0.132	Lymphoid Tissue	2155	166-1938	590	66532.5	Identities 497/582 (85%); Positives 536/582 (92%) with ACC:Q64151 Semaphorin I (M-SEMA FA Factor in Neural Network Develooment) *Mus musculus*. 834 amino acid residues.	Identities 247/506 (48%); Positives 330/506 (65%) with ACC:Q92854 Semaphorin *Homo sapiens*. 862 Amino Acid residues.	yyyy. Most likely cleavage site between positions 20and 21: GIG-AE.	Microbody (Peroxisome)- Cert.=7480. Appears to possess a cleavable N-terminal Signal Sequence.
7	20422974_2	Lymphoid Tissue	2284	166-1956	596	66969.8	Identities 498/585 (85%); Positives 540/585 (92%) with ACC:Q64151 Semaphorin I (M-SEMA FA Factor in Neural Network Development) *Mus musculus*. 834 amino acid residues.	Identities 265/558 (47%); Positives 353/558 (63%) with ACC:Q92854 Semaphorin *Homo sapiens*. 862 Amino Acid residues.	yyyy. Most likely cleavage site between positions 20and 21: GIG-AE.	Microbody (Peroxisome)- Cert.=7480. Appears to possess a cleavable N-terminal Signal Sequence.
8	20936375.0.1	Kidney	1930	148-1758	536	60306.7	Identities 453/531 (85%); Positives 482/531 (90%) with ACC:P07106 Bovine DBI-Related Brain Membrane Protein.	Identities 37/91 (40%); Positives 58/91 (63%) with ACC:O75521 DBI-Relted Protein *Homo sapiens*. 364 Amino acid residues.	nnny. Most likely cleavage site between positions 15 and 16:SWC-CC.	Plasma Membrane - Cert.=0.7000. Appears to possess a cleavable N-terminal Signal Sequence.
9	20936785.0.1	Brain, Fetal Brain	930	123-626	167	18440	Identities 167/167 (100%) with Human Transmembrane Protein HTMPN-46.	Identities 167/167 (100%) with Human Transmembrane Protein HTMPN-46.	nnny. Most lkely cleavage site between positions 31 and 32:TPR-LS.	Plasma Membrane - Cert.=64000. Appears to possess an uncleavable N-terminal Signal Sequence. Likely a Type IIIa Mmebrane Protein

Fig. 20B

SEC No.	Clone Number	Tissue Expression	Nucleo tide Length	ORF	Amino Acid Length	Calculated Molecular Weight	Protein Similarity (BLASTP Non-Redundant Composite Database)	Protein Similarity (Human Sequence)	Signal Peptide Cleavage Site (nt)	Cellular Localization
10	1795045. 0.77	Brain. Thalamus	1737	296-1690	464	51645.6	Identities 51/198 (25%); Positives 71/198 (35%) with ACC:O00276 Lymphocyte-Associated Receptor of Death 2 *Homo sapiens*. 510 amino acid residues.	Identities 51/198 (25%); Positives 71/198 (35%) with ACC:O00276 Lymphocyte-Associated Receptor of Death 2 *Homo sapiens*. 510 amino acid residues.		Cytoplam- Cert.=0.4500. Appears to possess no cleavable N-terminal Signal Sequence.
11	20422974 .0.132_ex t2	Lymphoid Tissue, Aorta, Breast, Colon, Foreskin, Germ Cell, Muscle, Prostate, Spleen, Stomach, and Uterus.	2156	166-2040	624	70478.1	Identities 501/599 (83%); Positives 542/599 (90%) with ACC:Q92854 Semaphorin *Homo sapiens*. 862 Amino Acid residues.	Identities 501/599 (83%); Positives 542/599 (90%) with ACC:Q92854 Semaphorin *Homo sapiens*. 862 Amino Acid residues.	yyyy. Most likely cleavage site between positions 20 and 21: GIG-AE.	Microbody (Peroxisome)- Cert.=7480. Appears to possess a cleavable N-terminal Signal Sequence.
12	20936375 .0.104	Kidney	1930	7-1611	534	60037.3	Identities 453/531 (85%); Positives 482/531 (90%) with ACC:P07106 Bovine DBI-Related Brain Membrane Protein.	Identities 37/91 (40%); Positives 58/91 (63%) with ACC:O75521 DBI-Related Protein *Homo sapiens*. 364 amino acid residues.		Plasma Membrane - Cert.=0.7300. Appears not to possess a cleavable N-terminal Signal Sequence.

Fig. 20C